PDB annotation		OXIDOREDUCTASE COX-2, CYCLOOXYGENASE, PROSTAGLANDIN, ARACHIDONATE, 2 ENDOPEROXIDE	OXIDOREDUCTASE HEME- PROTEIN, PEROXIDASE, OXIDOREDUCTASE, PEROXIDASE- 2 BROMIDE COMPLEX	OXIDOREDUCTASE HEME- PROTEIN, PEROXIDASE, OXIDOREDUCTASE, PEROXIDASE-2 BROMIDE COMPLEX	OXIDOREDUCTASE ARACHIDONIC ACID, MEMBRANE PROTEIN, PEROXIDASE, DIOXYGENASE		OXIDOREDUCTASE ADR, NADPH: ANDRENDIOXIN OXIDOREDUCTASE; FLAVORNZYME, MAD ANALYSIS, ELECTRON TRANSFERASE	OXIDOREDUCTASE FLAVOPROTEIN, OXIDASE	TO MODER DELOTES COMPLEX II. COMPLEX II. COMPLEX II. COMPLEX II. FINARAT II. SUCCIAAT EBENCHAS, COMPLEX II. SUCCIAAT EBENDEOGENSE, 2 RESPIRATION, OXIDOREDUCTARE
Coumpound	2CBA 4	PROSTAGLANDIN H2 SYNTHASE-2; CHAIN: A, B; 9- MER; CHAIN: F;	MYELOPEROXIDASE; CHAIN: A, B, MYELOPEROXIDASE; CHAIN: C, D;	MYELOPEROXIDASE; CHAIN: A, B; MYELOPEROXIDASE; CHAIN: C, D;	PROSTAGLANDIN H2 SYNTHASE-1; CHAIN: A;		ADRENODOXIN REDUCTASE; CHAIN: A;	SARCOSINE OXIDASE; CHAIN: A, B;	ILMANATE REDUCTASE FLAVOROTEN SUBUNT; CHANE, A FUMARATE REDUCTASE IRON-SULFUR PROTENC-CHANE, B, FUMARATE FROM ANTER REDUCTASE 18 CD HYDROPHOBIC PROTEN; KEDUCTASE 18 KD KEDUCTASE 18 KD
SEQFOL D score									
PMF		-0.11	0.19	1.00	1:00		0.00	0.81	0.03
Verify		0.06	-0.76	0.61	0.22		-0.65	0.31	-0.04
Psi Blast		0	3.4e-41	0	0		0.0045	6.8e-37	8.5e-53
END		089	241	714	089		23	430	437
STAR T AA		167	139	252	167		21	62	19
CHAI N ID		<	∢	O O	∢		∢	V	<
EDE EDE		levu	1d2v	1d2v	ldiy		Icje	lel5	1fum
SEQ ON ON		1568	1568	1568	1568	П		1569	1569

PDB annotation			OXDOREDUCTASTS FUMARATE REDUCTASTS, SUCCINATE DEHYDROGENASTS, RESPIRATORY 2 CHAN, CITRIC AGID CYCLE, TAVOPROTENIN RON-SULPHUR 3 PROTEIN, DIHAEM CYTOCHROME B	OXIDOREDUCTASE OXIDOREDUCTASE		ACTIN-BINDING PROTEIN ACTIN- BINDING PROTEIN, CALCIUM- BINDING, PHOSPHORY I, ATION	ACTIN-BINDING PROTEIN ACTIN- BINDING PROTEIN, CALCIUM- BINDING, PHOSPHORY I ATTON	STRUCTURAL PROTEIN CALPONIN HOMOLOGY, ACTIN BINDING, STRUCTURAL PROTEIN	STRUCTURAL PROTEIN CALPONIN
Coumpound	HYDROPHOBIC PROTEIN; CHAIN; D, P;	OXIDOREDUCTASE DIHYDROLIPOAMIDE DEHYDROGENASE (E.C.18.1.4) COMPLEX WITH 1LPF 3 FLAVIN-ADBRING. DINUCLEOTIDE (FAD) 1LPF 4	FUMAKATE KEDÜCTASIE FLAVOROTEIN SUBUNIT; CHAIN: A. D. FUMAKATE REDÜCTASIE RION-SULEUR PROTEIN, CHAIN: B. E. FUMAKATE REDÜCTASIE FUMAKATE REDÜCTASI CHAIN: C. E. FUMAKATE REDÜCTASI CHAIN: C. E.	FLAVOCYTOCHROME C3 FUMARATE REDUCTASE; CHAIN: A, D;	OXIDOREDUCTASE DIHYDROLIPOAMIDE DEHYDROGENASE (E.C.1.8.1.4) 3LAD 3	T-FIMBRIN; CHAIN: NULL;	T-PIMBRIN; CHAIN: NULL;	UTROPHIN; CHAIN: A, B;	UTROPHIN; CHAIN: A, B;
SEQFOL D score							·	74.32	
PMF		0.07	0.04	60:0-	60.0	0.83	0.40		1.00
Verify		-0.23	-0.34	0.04	-0.09	0.60	0.54		0.84
Psi Blast		0.003	1.2e-43	8.5e-29	0.0015	5.1e-24	1.5e-29	4.5e-35	1.7e-34
END AA		28	437	434	83	230	230	232	232
STAR		46	19	28	46	125	127	123	126
CHAI N ID		∢	₹ .	Ą	Ą			<	Ą
PDB ID		1lpf	lqia	1908	3lad	Iaoa	Iaoa	1bhd	1bhd
SEQ NO:		1569	1569	1569	1569	1571	1571	1571	1571

-	EDB 1D	CHAI	STAR T AA	END	Psi Blast	Verify score	PMF	SEQFOL D score	Coumpound	PDB annotation
1	\top									HOMOLOGY, ACTIN BINDING, STRUCTURAL PROTEIN
15	1bhd	∢	127	232	4.5e-35	0.85	1.00		UTROPHIN; CHAIN: A, B;	STRUCTURAL PROTEIN CALPONIN HOMOLOGY, ACTIN BINDING, STRUCTURAL PROTEIN
さ	格	<	126	235	8.5e-43			86.88	SPECTRIN BETA CHAIN; CHAIN: A;	ACTIN-BINDING CALPONIN HOMOLOGY (CH) DOMAIN; FILAMENTOUS ACTIN-BINDING DOMAIN, CYTOSKELETON
蓝	1bkr	<	127	235	8.5e-43	0.86	1.00		SPECTRIN BETA CHAIN; CHAIN: A;	ACTIN-BINDING CALPONIN HOMOLOGY (CE) DOMAIN; FILAMENTOUS ACTIN-BINDING DOMAIN, CYTOSKELETON
	1dxx	∢	126	233	le-35	0.69	0.1		DYSTROPHIN; CHAIN: A, B, C, D;	STRUCTURAL PROTEIN DYSTROPHIN, MUSCULAR DYSTROPHY, CALPONIN HOMOLOGY DOMAIN, 2 ACTIN- BINDING, UTROPHIN
lä-	Iqag	4	126	233	5.1e-35	0.68	1.00		UTROPHIN ACTIN BINDING REGION; CHAIN: A, B;	STRUCTURAL PROTEIN CALPONIN HOMOLOGY DOMANIN, DOMAIN SWAPPING, ACTIN BINDING, 2 UTROPHIN, DYSTROPHIN, STRUCTURAL PROTEIN
	lc4z	A	202	562	0	0.24	1.00		UBIQUITIN-PROTEIN LIGASE E3A; CHAIN: A, B, C; UBIQUITIN CONJUGATING ENZYME E2: CHAIN: D:	LIGASE E6AP; UBCH7; BILOBAL STRUCTURE, ELONGATED SHAPE, E3 UBIQUITIN LIGASE, E2 2 UBIQUITIN CONUGATING ENZYME
	lo4z	∢	212	564	0			131.07	UBIQUITIN-PROTEIN LIGASE E3A, CHAIN: A, B, C, UBIQUITIN CONUGATING ENZYME E2, CHAIN: D,	LIGASE EGAP, UBCHT, BILOBAL STRUCTURE, ELONGATED SHAPE, E3 UBIQUITIN LIGASE, E2 2 UBIQUITIN CONJUGATING ENZYME
	Jdaj	A	115	202	1e-06	99.0	0.05		NEURAL CELL ADHESION	CELL ADHESION NCAM; NCAM,

		50	I	2 2	Ä,	1X.F	1X.		П		Γ
PDB annotation	IMMUNOGLOBULIN FOLD, GLYCOPROTEIN	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGPS, FGR2, MAGINOGLOBULIN (IGLIKE DOMAINS BELONGING TO THE L SET 2 SUBGROUP WITHIN IGLIKE DOMAINS R-TREFOIL FOLD		IMMUNOGLOBULIN-LIKE DOMAIN CONNECTIN 127, TITIN IG REPEAT 27; MUSCLE PROTEIN, IMMUNOGLOBULIN-LIKE DOMAIN	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM	TRANSFERASE DINUCLEOTIDE- BINDING MOTIF, PHOSPHORIBOSYL TRANSPERASE	TRANSFERASE DINUCLEOTIDE- BINDING MOTIF, PHOSPHORIBOSYL TRANSFERASE	HYDROLASE NEURAMINIDASE; HYDROLASE, GLYCOSIDASE	HYDROLASE NEURAMINIDASE; HYDROLASE, GLYCOSIDASE	HORMONE/GROWTH FACTOR HORMONE, RECEPTOR, HORMONE/GROWTH FACTOR	HORMONE/GROWTH FACTOR HORMONE RECEPTOR
-				8088	E E	HMH	H M H	HH	шш	田田田	HH
Coumpound	MOLECULE; CHAIN: A, B, C, D;	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	TLYMPHOCYTE ADHESION GLYCOPROTEIN CD2 (RAT) 1HNG 3	TITIN, 127; CHAIN: NULL;	PC GAMMA RIIB; CHAIN: A;	NICOTINATE MONONUCLEOTIDE:5,6- CHAIN: A:	NICOTINATE MONONUCLEOTIDE:5,6- CHAIN: A:	SIALIDASE; CHAIN: NULL;	SIALIDASE; CHAIN: NULL;	GROWTH HORMONE; CHAIN: A; PROLACTIN RECEPTOR; CHAIN: B:	GROWTH HORMONE; CHAIN: A: PROLACTIN RECEPTOR:
SEQFOL D score											53.09
PMF		0.13	0.04	0.00	0.01	-0.19	-0.20	-0.20	-0.19	-0.14	
Verify		-0.30	0.13	-0.25	0.13	80:0	0.14	90.0	0.03	0.02	
Psi Blast		3e-05	1.5e-06	1.2e-05	7.5e-06	9e-10	7.5e-10	1.5e-10	6e-10	6e-11	6e-11
END		881	212	186	206	999	643	324	476	212	224
STAR		1113	115	113	105	484	491	138	266	102	31
CHAI		ii.	e e		v	V	Ą			g	В
en En		lev2	Ihng	1tit	2fcb	140s	IdOs	lent	leut	1bp3	1bp3
SEQ NO		1575	1575	1575	1575	1576	1576	1576	1576	1578	1578

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PDB annotation	HORMONE/GROWTH FACTOR	CONNECTIN 471, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III	MEMBRANE PROTEIN BETA SANDWICH, CYTOKINE RECEPTOR, FN3 DOMAIN		HORMONE/GROWTH FACTOR/HORMONE/RECEPTOR 4- HELLCAL BUNDLE, ALPHA HELLCAL BUNDLE, TERNARY COMPLEX, FN 2 III DOMAINS, BETA SHEET DOMAINS, CTTOKINE-	HEPARIN AND INTEGRIN BINDING HEPARIN AND INTEGRIN BINDING	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLUIAR MATRIX, 2 HEPARIN-BINDING, GLYCOROTEIN	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING,
Coumpound	CHAIN: B;	TITIN; CHAIN: NULL;	CYTOKINE RECEPTOR COMMON BETA CHAIN; CHAIN: A;	MOLECULE DROSCOPHILA MOLECULE DROSCOPHILA NELROGIAMA CONTAINING THE ICES 3 TWO AMINO PROZMALL FIBRONECTIN TYPE II PEREZPIS ICES 4 (RESDUES (10 - 81.4) ICES 5	PLAGENTAL LACTOGEN; CHAIN: A; PROLACTIN RECEPTOR; CHAIN: B, C;	FIBRONECTIN; CHAIN: A;	FIBRONECTIN; CHAIN: NULL;	FIBRONECTIN; CHAIN: NULL;
SEQFOL D score						56.61	57.30	
PMF		-0.08	-0.09	0.04	-0.14			0.34
Verify		-0.00	80.0	0.09	0.23			0.30
Psi Blast		9e-10	3e-08	6e-10	3e-10	7.5e-06	1.2e-09	1.2e-09
END		218	211		211	315	224	199
STAR T AA		119	124	41	124	35	34	37
CHAI N ID			∢		щ	٧		
EDB CI		1bpv	108p	lofb	1f6f	1fuh	lmfn	Imfn
SEQ NO:		1578	1578	1578	1578	1578	1578	1578
				704				

PDB annotation	GLYCOPROTEIN	STRUCTURAL PROTEIN TENASCIN, FIBROMECTIN TYPE-III, HEPARIN, EXTRACELLUIAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN		PROTEIN BINDING ED-B, FIBRONECTIN, TYPEII DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING	TRANSFERASE ACETYLTRANSFERASE	TRANSFERASE AMINOGLYCOSIDE 3-N-ACETYLTRANSFERASE, EUBACTERIAL 2 AMINOGLYCOSIDE RESISTANCE, GCNS-RELATED N-	ACETYLTRANSFERASE, 3 COA- BINDING	TRANSFERASE N-ACETYL. TRANSFERASE	TRANSFERASE PROTEIN-ACETYL COENZYME A COMPLEX, ACETYLTRANSFERASE	TRANSFERASE PROTEIN-ACETYL COENZYME A COMPLEX, ACETYLTRANSFERASE	
Coumpound		TENASCIN; CHAIN: A, B;	GLYCOPROTEIN FIBRONECTIN (TENTH TYPE III MODULE) (NMR, 36 STRUCTURES) ITTF 3	FIBRONECTIN; CHAIN: A;	ARYLALKYLAMINE N- ACETYLTRANSFERASE; CHAIN: A, B;	SERRATIA MARCESCENS AMINOGLYCOSIDE-3-N- CHAIN: A, B;		SEROTONIN N- ACETYLTRANSFERASE; CHAIN: A;	HPA2 HISTONE ACETYLTRANSFERASE; CHAIN: A, B, C, D;	HPA2 HISTONE ACETYLTRANSFERASE; CHAIN: A, B, C, D;	
SEQFOL D score		55.27									
PMF			0.59	0.10	0.80	0.10		98.0	0.04	00:00	
Verify score			-0.03	0.11	0.42	-0.56		0.50	-0.15	0.08	
Psi Blast		4.5e-07	1.5e-09	9e-10	8.5e-14	1.7e-10		5.1e-13	5.1e-12	1.5e-14	
END AA		211	199	213	627	622		627	624	633	_
STAR		35	124	124	511	523		511	487	537	_
CHAI N ID		∢		٧	В	⋖		٧	٧	٧	
EDB OI		lqr4	1mf	2fiib	1966	1604		1cjw	lqsm	1qsm	
SEQ NO D		1578	1578	1578	1579	1579		1579	1579	1579	

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PDB annotation	TRANSFERASE ACETYLTRANSFERASE	TRANSFERASE AAC; AMINOGLYCOSIDE 6-N- ACETYLTRANSFERASE, ANTIBIOTIC 2 RESISTANCE,	ACT TL CORACTOR TRANSFER AMENDARY TRANSFER AMENDARY TRANSFER AMENDARY AMENDARY AMENDARY TRANSFER AMENDARY AMENDARY ACETYLTRANSFER ASS, 3 COAMENDARY AMENDARY	TRANSFERASE N-ACETYL TRANSFERASE	SIGNALING PROTEIN P300/CBP ASSOCIATED FACTOR, COENZYME A, ACETYLTRANSFERASE, 2 COACTIVATOR, SIGNALING PROTEIN	TRANSFERASE PROTEIN-ACETYL COENZYME A COMPLEX, ACETYLTRANSFERASE	TRANSFERASE PROTEIN-ACETYL COENZYME A COMPLEX, ACETYL TRANSFER ASE	TRANSFERASE HISTONE ACETYLTRANSFERASE, GCNS- REATED N- ACETYLTRANSFERASE, 2 COA BUDING PROTEIN
Coumpound	ARYLALKYLAMINE N- ACETYLIRANSFERASE; CHAIN: A. B:	AMINOGLYCOSIDE N6'- ACETYLTRANSFERASE TYPE 1; CHAIN: A;	SERRATIA MARCESCENS AMINOGLYCOSIDE-3-N- CHAIN: A, B;	SEROTONIN N- ACETYLTRANSFERASB; CHAIN: A:	P300/CBP ASSOCIATING FACTOR; CHAIN: B, A;	HPA2 HISTONE ACETYLTRANSFERASE; CHAIN: A, B, C, D;	HPA2 HISTONE ACETYLTRANSFERASE; CHAIN: A. B. C. D:	TGCN5 HISTONE ACETYL TRANSFERASE; CHAIN: A;
SEQFOL D score								
PMF	0.83	0.16	0.04	0.63	0.10	0.64	0.00	0.48
Verify	0.43	-0.18	-0.18	0.59	0.13	0.17	80.0	-0.21
Psi Blast	3.4e-19	1.7e-11	5.1e-12	1.5e-18	1e-17	3.4e-11	1.5e-14	8.5e-16
END	732	749	727	732	751	729	738	749
STAR	919	979	627	019	637	519	642	637
CHAI N ID	8	∢	<	٧	В	¥.	∢	¥
PDB CI	1566	1587	1bo4	1cjw	1cm0	lqsm	1qsm	lqst
SEQ O	1580	1580	1580	1580	1580	1580	1580	1580

PDB annotation	GENE REGULATION ADAS: TRANSCRIPTIONAL REGULATION, HISTONE ACETYTATION, N. 2 ACETYTIANSPERASE, GCAS RELATED NACETYTIANSPERASE FAMILY, 3 GENE REGULATION	OXIDOREDUCTASE TRYPANOTHEONE REDUCTASE, FAD DEPENDENT DISULPHIDE 2 OXIDOREDUCTASE			RNA BINDING PROTEIN SNRNP, SPLICING, SPLICEOSOME, SM, CORE SNRNP DOMAIN, 2 SYSTEMIC LUPUS ERYTHEMATOSUS, SLE	RNA BINDING PROTEIN SNRNP, SPLICING, SPLICEOSOME, SM, CORE SNRNP DOMAIN, 2 SYSTEMIC LUPUS ERYTHEMATOSUS, SLE	RNA BINDING PROTEIN D3 CORE SNRNP PROTEIN; B CORE SNRNP PROTEIN SNRNP, SPLICING, SM, CORE SNRNP DOMAIN, SYSTEMIC LUPUS 2 ERYTHEMATOSUS, S.LE,
Coumpound	TRANSCRIFTIONAL ACTIVATOR GCN5; CHAIN: A, B;	TRYPANOTHIONE REDUCTASE; CHAIN: A, B;	POLYAMINE OXIDASE; CHAIN: A, B, C;	OXIDOREDUCTASE DIHYDROLIPOAMIDE DEHYDROGENASE (E.C.1.8.1.4) 3LAD 3	SWALL NUCLEAR RIBONUCLEOPROTEIN SM DI; CCHAIN: A; SMALL NUCLEAR RIBONUCLEOPROTEIN SM DZ; CHAIN: B;	SWALL NUCLEAR RIBONUCLEOPROTEIN SM DI; CHAIN: A; SMALL NUCLEAR RIBONUCLEOPROTEIN SM D2; CHAIN: B:	SMALL NÜCLEAR RIBONUCLEOPROTEIN SM D3; CHAIN: A, C, E, G, I, K; SMALL NUCLEAR RIBONUCLEOPROTEIN
SEQFOL D store							
PMF	0.39	0.21	60.0	0.16	0.63	0.93	0.33
Verify	-0.37	0.06	0.02	0.01	0.48	0.50	0.50
Psi Blast	5.16-14	1.2e-06	0.00014	1.5e-07	1.4e-13	3.46-11	1.7e-11
END	749	116	104	123	126	221	126
STAR	637	65	70	29	44	40	14
CHAI	∢	<	<	∢	<	В	∢
EDE EDE	lygh	laog	1637	3lad	1634	Ib34	1436
SEQ NO:	1580	1582	1582	1582	1587	1587	1587

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PDB annotation	RNA BINDING PROTEIN	RNA BINDING PROTEIN DS CORE SNRKP ROCHES, BOORS SNRNP PROTEIN SNRNP, SPLICING, SM, CORE SNRNP DOMAN, SYSTEMIC LUPUS 2 RKYTEMATOSUS, SLE, RNA BINDING PROTEIN	RNA BINDING PROTEIN DS CORE SINKIP BOCHES, BOGE SINKIP PROTEIN SINKIP, SPLICING, SM, CORE SINKIP DOMAIN, SYSTEMIC LUPUS 2 ERYTHEMATOSUS, SLE, RNA BINDING PROTEIN		OXIDOREDUCTASE PDZ DOMAIN, NNOS, NITRIC OXIDE SYNTHASE	OXIDOREDUCTASE PDZ DOMAIN, NNOS, NITRIC OXIDE SYNTHASE	PEPTIDE RECOGNITION PEPTIDE RECOGNITION, PROTEIN LOCALIZATION	CYTOKINE LCF; CYTOKINE, LYMPHOCYTE CHEMOATTRACTANT FACTOR, PDZ DOMAIN	KINASE HCASK, GLGF REPEAT, DHR; PDZ DOMAIN, NEUREXIN, SYNDECAN, RECEPTOR CLUSTERING, KINASE
Coumpound	ASSOCIATED CHAIN: B, D, F, H, J, L;	SMALL NUCLEAR RIBONUCLEOPROTEIN SM D3; CHANY, A, C, E, G, I, K, SMALL NUCLEAR RIBONUCLEOPROTEIN ASSOCIATED CHAIN: B, D, F, H, A1, Li,	SWALL NUCLEAR RIBONUCLEOPROTEIN SM D3; CHAIN: A, C, E, G, I, K; SMALL NUCLEAR RIBONUCLEOPROTEIN ASSOCIATED CHAIN: B, D, F, H, J, L;		NEURONAL NITRIC OXIDE SYNTHASE; CHAIN: A; HEPTAPEPTIDE; CHAIN: B;	NEURONAL NITRIC OXIDE SYNTHASE; CHAIN: A; HEPTAPEPTIDE; CHAIN: B;	PSD-95; CHAIN: A; CRIPT; CHAIN: B;	INTERLEUKIN 16; CHAIN: NULL;	HCASK/LIN-2 PROTEIN; CHAIN: A, B;
SEQFOL D score									
PMF		0.99	0.69		0.96	0.82	00'1	0.76	0.93
Verify		0.25	0.26		69'0	0.72	0.56	0.35	0.83
Psi Blast		5.1e-24	8.5e-25		3e-14	3.4e-13	1.5e-18	1.5e-16	7.5e-15
END		134			80	110	98	%	82
STAR T AA		8	39		12	9	5	6	6
CHAI N ID		щ	Д		A	¥	¥		¥
PDB ID		1d3b	1436		1b8q	1689	1be9	1116	Ikwa
SEQ NO:		1587	1587		1588	1588	1588	1588	1588

PDB annotation	SIGNAL TRANSDUCTION HDLG, DHR3 DOMAIN; SIGNAL TRANSDUCTION, SH3 DOMAIN, REPEAT	OXIDOREDUCTASE BETA-FINGER	MEMBRANE PROTEINOXIDOREDUCTASE BETA- FINGER, HETERODIMER	PEPTIDE RECOGNITION PSD-95, PDZ DOMAIN, NEURONAL NITRIC OXIDE SYNTHASE, NMDA RECEPTOR 2 BINDING	HYDROLASE PDZ DOMAIN, HUMAN PHOSPHATASE, HPTP1E, PTP-BAS, SPECIFICITY 2 OF BINDING	PROTEIN BINDING GATE-16; UBIQUITIN FOLD	LIPID TRANSPORT APO A-I; LIPOPROTEIN, LIPID TRANSPORT, CHOLESTEROL METABOLISM, 2 ATHEROSCLEROSIS, HDI, LCAT- ACTIVATION	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN
Coumpound	HUMAN DISCS LARGE PROTEIN; CHAIN: NULL;	NEURONAL NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: A;	ALPHA-I SYNTROPHIN (RESIDUES 77-171); CHAIN: A; NEURONAL NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: B;	POSTSYNAPTIC DENSITY PROTEIN 95; CHAIN: A;	TYROSINE PHOSPHATASE (PTP-BAS, TYPE I); CHAIN: A;	GOLGI-ASSOCIATED ATPASE ENHANCER OF 16 KD; CHAIN: A, B;	APOLIPOPROTEIN A-1; CHAIN: A, B, C, D;	ALPHA SPECTRIN; CHAIN: A, B, C;
SEQFOL D score					And a second second		54.19	61.70
PMF	00'1	0.95	1.00	66:0	1:00	0.89		
Verify	0.78	0.89	99.0	62:0	0.91	0.36		
Psi Blast	le-17	1.2c-14	3.4e-19	1.46-15	1.7e-16	8.5e-34	4.5e-06	1.5e-07
END	8	96	18	8	98	187	244	248
STAR T AA	e.	12	3	_	я	16	29	28
CHAI		V V	¥	∢	V V	< −	. 4	4
10B	1pdr	lgau	1qav	1qlc	3pqz	1606	lavI	lcun
S B S	1588	1588	1588	1588	1588	1590	1651	1591

PDB annotation	ENDOCYTOSIS/EXOCYTOSIS NSECI; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT	MEMBRANE PROTEIN FOUR HELLY BUNDLE, ALPHA HELIX	CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL, CONTRACTILE PROTEIN	TRANSPORT PROTEIN YAMP 2; MEMBRANE FUSION PROTEIN COMPLEX, TRANSPORT PROTEIN	DESIGNED HELICAL BUNDLE DESIGNED HELICAL BUNDLE	DESIGNED HELICAL BUNDLE DESIGNED HELICAL BUNDLE	COMPLEX (BLOOD COACULATION/HIBITOR) AUTOPROTHENBENE HYDROLASE, SERUE HYDROLASE, SERUE HYDROLASE, SERUE BROTENASE, PLASMA CALCUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD	COMPLEX (RLOOD COAGULATION/NHIBITOR) AUTOROTHROMBIN IIA; HYDROLASE, SERINE PROTEIN/SESI, PLASAR CALCIUM BINDING, 2 GLYCOPROTEIN,
Commpound	SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	SSOI PROTEIN; CHAIN: A;	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	SYNAPTOBREVIN 2; CHAIN: A, E, I; SYNTAXIN 1A; CHAIN: B, F, J; SNAP-25B; CHAIN: C, G, K; SNAP-25B; CHAIN: D, H, L;	DHP1; CHAIN: NULL;	DHP1; CHAIN: NULL;	ACTIVATED PROTEIN C, CHAIN: P, D-PHE-PRO-MAI, CHAIN: P,	ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;
SEQFOL D score				57.26	55.15				
PMF	0.45	0.95	0.04			0.16	0.17	90.0	0.47
Verify	-0.00	0.16	0.23			0.49	0.17	0.21	0.32
Psi Blast	3.4e-22	1.5e-38	3.4e-13	4.5e-12	9e-24	5.1e-05	3.4e-05	16-10	4.5e-12
END	233	233	213	251	245	73	75	324	385
STAR	- 21	19	22	28	174	30	36	249	306
CHAI	В	В	Ą	Ą	м			_	H
PDB	ldnl	ldn1	1fio	lquu	lsfc	4hb1	4hb1	laut	lant
SEQ NO DE	1651	1651	1591	1591	1591	1591	1591	1592	1592

PDB annotation	COMPLEX (BLOOD COAGULATION/INHIBITOR)	SUBFACE PROTEIN MEROZÓTTE SURFACE ANTIGEN I, MAJOR BLOOD-STAGE GEF-LIKE DOWANN, EXTRACELULAR, MODULAR PROTEIN, SURFACE 2 ANTIGEN, MALLARIA VACCINE COMPONENT, SUBFACE DE OCURO	SURFACE PROTEIN MEROZOTTE SURFACE ANTIGEN! I. MAJOR BLOOD-STAGE EGF-LIXE DOMAN, EXTRACELULAR, MODULAR PROTEN, SURFACE 2 ANTIGEN, MALARIA VACCINE COMPONENT; SURFACE PROTEIN	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, COFACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)	BLOOD COAGULATION, SERNE PROTEAS, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INTIBITION, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)	BLOOD COAGULATION, SERINE PROTEASE, COAPLEZ, COFACTOR, 2 RECEPTOR ENZYNE, INHBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTIOR/LIGAND)
Coumpound		MEROZOITE SURFACE PROTEIN 1; CHAIN: A;	MEROZOITE SURFACE PROTEIN I; CHAIN: A;	BLOOD COAGULATION PACTOR VIIA; CHAIN: I., H; SOLUBLE TISSUE PACTOR; CHAIN: T, U; DPHE-PHE-ARG- CHLOROMETHYLKETONE CHLOROMETHYLKETONE	BLOOD COAGULATION FACTOR VILA; CHAIN: L, H; SOLUBLE TISSUE PACTOR; CHAIN: T, UJ D-PHE-PHE-ARG- CHLOROMETHYLKETONE CHLOROMETHYLKETONE CHLOROW WITH CHAIN: C;	BLOOD COAGULATION FACTOR VIIA; CHAIN: I., H; SOLUBLE TISSUE PACTOR; CHAIN: I. U; D-PHE-PHE-ARG- CHLOROMETHYLKETONE CHLOROMETHYLKETONE
SEQFOL D score	A Constitution of the Cons					
PMF		0.04	0.04	0.09	-0.19	0.16
Verify		0.18	0.06	0.44	0.17	0.02
END Psi Blast AA		1.5e-09	1.56-14	1.4e-09	3.4e-11	3e-15
END		326	374	186	249	385
STAR		246	280	109	139	253
CHAI N ID		<	<	J	<u>.</u>	٦
802 ED		lcej	leel	Idan	1dan	1dan
SEQ NO:		1592	1592	1592	1592	7651

PDB annotation	HYDROLASE/HYDROLASE NHBITOR PROTEIN-PEPTIDE COMPLEX	HYDROLASE/HYDROLASE NHBBTOR PROTEIN-PEPTIDE COMPLEX	SERNE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II; ESTONOUCLIN, TA, CD14 ANTIGENS, EGR-CMS, SERINE PROTEINASE, EGR-LIKE DOMANS, ANTIGENSOUTHAT COMPLEX, 2 ANTIGENSOUTHAT COMPLEX, 2	SERINE PROTEINASE COAGULATION FACTOR II, COAGULATION FACTOR II, ESTONODULIN TA CDI41 ANTIGENE EGC-CAKK SERINE RATTGENE, EGC-CAKK SERINE RATTGENE, EGC-LIKE DOMAINS, ANTIGOAGULANI TO COMPLEX, ANTIGOAGULANI COMPLEX, ANTIGENE	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, CLI CYCOPROTEIN, 2 REPEAT, SIGNAL, MUTTIGENE FAMILY, DISRASE MITATION, 3 EGP-LIKE
	HYDROLA INHIBITOI COMPLEX	HYDROLA INHIBITOI COMPLEX	SERIN COAG COAG COAG FETON ANTIG ANTIG	SERIN COAG COAG EETON ANTIG PROTE ANTIG	MATR EXTRA CALCI GLYCC SIGNA DISEAS
Coumpound	DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I, DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)- PHE-ARG, CHAIN: C, D; PPETTIE E-Y, CHAIN: X, Y;	DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I, DES-GLA FACTOR VIIA (LIGHT CHAIN; CHAIN: L, M; (DPN)- PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAYY CHAIN, CHAIN: M, N, P; THROMBOMODULIN; CHAIN: I, K, I; THROMBIN INHIBITOR L-GLU-L-GLY-L ARM; CHAIN: E, F, G, H;	THROMBIN LIGHT CHAIN; CHAIN A, B, C, D, THROMBIN HEAYY CHAIN, CHAIN, M, N, P, THROMBOMODILIN; CHAIN, I, K, I, THROMBIN INHIBITOR L-GLU-L-GLY-L ARM; CHAIN: B, F, G, H;	FIBRILLIN; CHAIN: NULL;
SEQFOL D score					
PMF	-0.03	-0.18	0.01	-0.15	-0.05
Verify score	0.24	0.13	-0.18	0.03	0:01
END Psi Blast AA	1.4e-09	3.4e-11	1.2e-14	8.5e-12	1.7e-09
	186	249	383	402	339
STAR T AA		139	295	307	245
CHAI N ID	ı	٦	н	_	
PDB UD	Idva	Idva	1dx5	1dx5	lemn
SEQ No ed	1592	1592	1592	1592	1592

PDB annotation	DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCHIM-BINIDING	GLYCOPROTEIN, 2 REPEAT,	DISEASE MUTATION, 3 EGF-LIKE	DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN	MATRIX PROTEIN	EXTRACELLULAR MATRIX,	GLYCOPROTEIN, 2 REPEAT.	SIGNAL, MULTIGENE FAMILY,	DISEASE MUTATION, 3 EGF-LIKE	FRAGMENT, MATRIX PROTEIN	MATRIX PROTEIN	EXTRACELLULAR MATRIX,	CALCIUM-BINDING,	GLYCOPROTEIN, 2 REPEAT,	SIGNAL, MULTIGENE FAMILY,	DISEASE MUTATION, 3 EGF-LIKE	DOMAIN, HUMAN FIBRILLIN-1	FRAGMENT, MATRIX PROTEIN	SIGNALLING PROTEIN BINDING	PROTEIN, CYTOKINE, SIGNALLING PROTEIN	BLOOD CLOTTING	COMPLEX(SERINE	PROTEASE/COFACTOR/LIGAND),	BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR,
Coumpound		FIBRILLIN; CHAIN: NULL;				FIBRILLIN; CHAIN: NULL;						FIBRILLIN; CHAIN: NULL;							TINGE SHOULD BY STORY	LUMOIC INECKOSIS FACTOR	RECEPTOR; CHAIN: A, B;	BLOOD COAGULATION	FACTOR VIIA; CHAIN: L;	BLOOD COAGULATION	FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR;
SEQFOL D score		56.86																	26.46	25.40					
PMF						0.55						0.13										0.03			
Verify						0.33						0.36										0.10			
Psi Blast		1.7e-15				1.7e-15						8.5e-14							20 10	26-10		1.4e-09			
END AA		382				380						402							257	<u> </u>		186			
STAR T AA		277				302						337							101	124		109			
CHAI																			<	4		L			
EDB ID		lemn				lemn						Iemn							lovi	TOVE		1fak			
SEQ NO.		1592				1592						1592							1502	1032		1592			

			_		_	_	_	_	_	_			_		,
PDB annotation	RECEPTOR ENZYME, 3 INHIBITOR, GLA, BGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING	LOOD CLOTTING COMPLEXION TO COMPLEXION TO COMPLEXION TO COMPLEX CONTRACTOR TO COMPLEX CONTRACTOR TO COMPLEX CONTRACTOR TO COMPLEX COMPLEX COMPLEX COMPLEX COMPLEX COMPLEX COMPLEX COMPLEX (CERINE 4 DETASE COMPLEX (COMPLEX (CERINE 4 DETASE COMPLEX (HORMONE RECEPTOR HORMONE RECEPTOR, INSULIN RECEPTOR FAMILY	GLYCOPROTEIN GLYCOPROTEIN	COMPLEX (BLOOD	COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX,	INHIBITOR, HEMOPHILIA/EGF,	SERINE PROTEASE, CALCIUM-	BINDING, HYDROLASE, 3	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR: COMPLEX.					
Coumpound	CHAIN: T; SLI5; CHAIN: 1;	EACTOR VIA, CEADIN. I, BLOOD COAGULATION BLOOD COAGULATION FACTOR VIA, CEADIN. H, SOLUBLE TISSUE FACTOR, CHAIN: T, SLIS, CHAIN. I,	INSULIN-LIKE GROWTH FACTOR RECEPTOR 1; CHAIN: A:	LAMININ; CHAIN: NULL;	LAMININ; CHAIN: NULL;	LAMININ; CHAIN: NULL;	LAMININ; CHAIN: NOLL;	LAMININ; CHAIN: NULL;	LAMININ; CHAIN: NULL;	FACTOR IXA; CHAIN: C, L,; D-	PHE-PRO-ARG; CHAIN: I;				FACTOR IXA; CHAIN: C, L.; D- PHE-PRO-ARG; CHAIN: I;
SEQFOL D score							70.13								
PMF		-0.18	0.00	0.31	-0.12	0.14	-0.10	-0.14	-0.19	-0.12					-0.07
Verify		0.08	0.20	0.15	0.44	0.29	61.0	0.37	20.0	0.58					0.44
Psi Blast		3.4e-11	4.5e-12	3.4e-I3	3.4e-18	7.5e-19	7.5e-19	3.4e-12	le-II	3.4e-09					1.5e-10
END		249	380	242	281	331	396	193	403	173					229
STAR T AA			246	112	146	220	231	27	295	109					139
CHAI		_1	<							r					J
90 E E		Ifak	1igr	1klo	1klo	Iklo	Iklo	1klo	1klo	1pfx					yjd1
SEQ NG EL		1592	1592	1592	1592	1592	1592	1592	1592	1592					1592

PDB annotation	INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3 GLYCOPROTEIN	SERINE PROTEASE FYIIA; BLOOD COAGULATION, SERINE PROTEASE	SERINE PROTEASE FVIIA; BLOOD COAGULATION, SERINE PROTEASE	SERINE PROTEASE FVIIA; BLOOD COAGULATION, SERINE PROTEASE	SERINE PROTEASE FVIIA; BLOOD COAGULATION, SERINE PROTEASE	PLASMINOGEN ACTIVATION	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD
Coumpound		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYI, INHIBITOR; CHAIN: C,	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL, INHIBITOR; CHAIN: C;	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	COAGULATION FACTOR VIIA (JGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEBYTY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	T-PLASMINOGEN ACTIVATOR F1-G; 1TPG 7 CHAIN: NULL; 1TPG 8	BLOOD COAGULATION FACTOR XA; CHAIN: L, C;
SEQFOL D score							
PMF		-0.09	-0.17	-0.18	0.71	-0.05	-0.12
Verify score		0.55	0.23	0.26	0.49	0.91	0.23
Psi Blast		1.4e-09	3.4e-10	7.5e-09	1.36-11	3e-10	3.4e-09
END		981	249	338	385	180	681
STAR T AA		109	143	253	283	128	109
CHAI		7	7	ı	1		1
PDB		Iqfk	1qfk	1qfk	Iqfk	ltpg	1xka
SEQ NO:		1592	1592	1592	1592	1592	1592

PDB annotation	COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD	COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD	COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN	BLOOD COAGULATION FACTOR	STUART FACTOR; BLOOD	COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2	GROWTH FACTOR LIKE DOMAIN		And the second s			-			CHAPERONE HSP40; CHAPERONE, HEAT SHOCK, PROTEIN FOLDING, DNAK
Coumpound		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	3 14 0	BLOOD COAGULATION F	FACTOR XA; CHAIN: L, C;	- 14	-	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ	LECTIN (AGGLUTININ) WHEAT	GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	LECTIN (AGGLUTININ) WHEAT	(ISOLECTIN 2) 9WGA 3	LECTIN (AGGLUTININ) WHEAT	(ISOLECTIN 2) 9WGA 3	DNAJ; CHAIN: NULL;
SEQFOL D score						53.26					60.84						81.78
PMF		-0.03		0.46						-0.12			-0.19		-0.05		
Verify score		90.04		0.43						0.22			0.04		-0.00		
Psi Blast		7.5e-09		1.2e-11		1.2e-11				3,4e-14	1.5e-16		1.4e-15		3.4e-13		3.4e-28
END		328		382		395				564	340		342		221		1.1
STAR T AA		255		283		305				411	152		183		92		1
CHAI N ID		г		Т		7				<	٧		٧		∢		
PDB		lxka		1xka		1xka				9wga	9wga		9wga		9wga		1bq0
SEQ NO:		1592		1592		1592				1592	1592		1592		1592		1593

PDB annotation .	NA (5'- TRANSCRIPTION FACTOR, DNA BINDING, DNA 2 BENDING, COMPLEX (HMG DOMAIN/DNA), GENE REGULATION/DNA		EIN 6 4; DNA BINDING PROTEIN HAG BOX, DNA BENDING, DNA RECOGNITION CHROMATIN, NMR, DNA 2 BINDING PROTEIN	S CHAIN: COMPLEX (DNA-BINDING Y 9 PROTEIN/DNA)	S CHAIN: COMPLEX (DNA-BINDING Y 9 PROTEIN/DNA)	COMPLEX (DNA-BINDING P. 9		COMPLEX (HMG DOMAIN'DNA), GENE REGULATION'DNA	-	
Coumpound	DNA (5'- CHAIN: B; DNA (5'- CHAIN: C;	LYMPHOID ENHANGER. BINDING FACTOR; CHAIN: A; DNA (\$'-CHAIN: B; DNA (\$'- CHAIN: C;	NON HISTONE PROTEIN 6 A; CHAIN: A;	HUMAN SRY; IHRY 6 CHAIN: A; IHRY 7 DNA; IHRY 9 CHAIN: B; IHRY 10	HUMAN SRY; IHRY 6 CHAIN: A; IHRY 7 DNA; IHRY 9 CHAIN: B; IHRY 10	HUMAN SRY; IHRY 6 CHAIN: A; IHRY 7 DNA; IHRY 9 CHAIN: B; IHRY 10	LYMPHOID ENHANCER- BINDING FACTOR; CHAIN: A; DNA (5'- CHAIN: B; DNA (5'-	Crain: C;	LYMPHOID ENHANCER- BINDING FACTOR: CHAIN: A:	DNA (%, CHAIN: B: DNA (%)
SEQFOL D score					83.75		57.47			
PMF		1.00	0.89	0.78		0.81			0.74	
Verify		0.40	0.10	-0.10		0.04			-0.29	
Psi Blast		3.4e-20	8.5e-21	16-21	7.5e-27	7.56-27	6e-27		8.5e-17	
END		420	8	114	115	115	128		128	
STAR		350	м	84	54	4	43		44	
CHAI N ID		Ą	<	V	¥	¥	Ą		٧	
PDB		2lef	1cg7	lhry	Ihry	lhry	2lef		2lef	
SEQ ID NO:		1594	1598	1598	1598	1598	1598		1598	

PDB annotation	COMPLEX (HMG DOMAIN/DNA), GENE REGULATION/DNA	GENE REGUL, TIONDAN LEF-1 HMG, LEF1, HMG, TCR-A, TRANSCRPTTON, PACTOR, DNA BINDING, DNA, 2 BENDING, COMPLEX (HMG DOMAIN/DNA), GENE REGUL, ATTOWIDNA	COMPLEX. TRANSDUCERTRANSDUCTION) OF BEFL-GAMMA, REKL, PF31; PHOSDUCIN, TRANSDUCIN, BETA- GAMMA, SIGNAL, TRANSDUCTION, SEGULATION, OF PROTEINS, PHOSPHORYLATION, OF PROTEINS, THOREDOXIN, STONI, MEKA, COMPLEX.	SH3 DOMAIN WW DOMAIN, FBP28, SIGNAL TRANSDUCTION	SH3 PROTOTYPE WWPROTOTYPE, PROTEIN DESIGN	SH3 PROTOTYPE WWPROTOTYPE, PROTEIN DESIGN	STRUCTURAL PROTEIN EF-HAND LIKE DOMAIN, WW DOMAIN			
Coumpound		LYMPHOID ENHANCER- BINDING FACTOR; CHAIN: A; DNA (5" CHAIN: B; DNA (5" CHAIN: C;	TRANSDUCIN; CHAIN: P;	FORMIN BINDING PROTEIN; CHAIN: A;	WWPROTOTYPE; CHAIN: A;	WWPROTOTYPE; CHAIN: A;	DYSTROPHIN; CHAIN: A;			
SEQFOL D score										
PMF		0.71	-0.20	96.0	0.94	06'0	86'0	0.87	0.35	0.22
Verify		0.27	0.10	09.0	0.72	0.17	60.0	0.03	0.64	0.27
Psi Blast		6e-27	1.5e-09	5.1e-07	1.5e-09	3e-09	8.5e-08	3.4c-09	3.4e-12	3.4e-06
END		116	173	160	191	121	121	159	118	117
STAR T AA		45	6	133	133	48	26	129	85	82
CHAI		A	o.,	٧	∢	A	Ą	V	٧	٧
PDB		2lef	2нс	1601	1601	1e0I	1e0I	Ie0m	1e0m	leg3
SEQ NO.		1598	1599	1602	1602	1602	1602	1602	1602	1602

u _o	DYL- NW INE	AIN, FBP28,	AIN, FBP28,	OTOTYPE,	OTOTYPE,	IDYL ww INE	ERASE, IDOXAL 5'-	SAT; L-SERINE	SAT; L-SERINE	ATE,	I.D	
PDB annotation	ISOMERASE PINI; PEPTIDYL- PROLINE ISOMERASE, WW DOMAIN, PHOSPHOSERINE BINDING	SH3 DOMAIN WW DOMAIN, FBP28, SIGNAL TRANSDUCTION	SH3 DOMAIN WW DOMAIN, FBP28, SIGNAL TRANSDUCTION	SH3 PROTOTYPE WWPROTOTYPE, PROTEIN DESIGN	SH3 PROTOTYPE WWPROTOTYPE, PROTEIN DESIGN	ISOMERASE PINI; PEPTIDYL. PROLINE ISOMERASE, WW DOMAIN, PHOSPHOSERINE BINDING	TRANSFERASE TRANSFERASE, METABOLIC ROLE, PYRIDOXAL 5'- PHOSPHATE	AMINOTRANSFERASE PSAT; AMINOTRANSFERASE, L-SERINE BIOSYNTHESIS	AMINOTRANSFERASE PSAT; AMINOTRANSFERASE, L-SERINE BIOSYNTHESIS	TRANSFERASE PSAT; AMINOTRANSFERASE, PYRIDOXAL-5'-PHOSPHATE, PHOSPHOSERINE, 2 ALKALIPHILIC	LYASE ALPHA/BETA FOLD	THE ASSESSMENT AND THE PROPERTY OF
Coumpound	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE NIMA- CHAIN: B; Y(SEP)PT(SEP)S PEPTIDE; CHAIN: C;	FORMIN BINDING PROTEIN; CHAIN: A:	FORMIN BINDING PROTEIN; CHAIN: A:	WWPROTOTYPE; CHAIN: A;	WWPROTOTYPE; CHAIN: A;	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE NIMA- CHAIN: B; Y(SEP)PT(SEP)S PEPTIDE; CHAIN: C;	SERINE HYDROXYMETHYLTRANSFER ASE; CHAIN: A;	PHOSPHOSERINE AMINOTRANSFERASE; CHAIN: A, B;	PHOSPHOSERINE AMINOTRANSFERASE; CHAIN: A, B:	PHOSPHOSERINE AMINOTRANSFERASE; CHAIN: A;	CSDB PROTEIN; CHAIN: A;	dramary.
SEQFOL D score								355.62				
PMF	0.01	0.82	0.94	66:0	0.99	0.01	0.78		1.00	1.00	1.00	05.0
Verify	-0.06	-0.19	0.72	0.25	0.25	-0.06	0.20		0.71	0.84	0.28	200
Psi Blast	90-99	1e-07	1.5e-09	6.8e-05	6e-05	90-99	1.7e-67	1.7e-58	1.7e-58	5.1e-60	1.7e-61	5 10.67
END AA	185	125	124	121	121	148	387	389	389	389	389	387
STAR	132	06	96	96	96	95	_	56	27	56	11	-
CHAI N ID	m	<	<	٧	٧	В	Ą	<	¥.	<	Ą	٧
EDB ID	1f8a	1601	1601	1c0m	1e0m	1f8a	15j4	16jn	16jn	1bt4	1c0n	0:01
No es Se	1602	1603	1603	1603	1603	1603	1606	1606	1606	9091	1606	9091

п	×	ERINE P.	ERINE-	ERASE, IDOXAL 5'-	SAT; L-SERINE	SAT;	ATE,	TD	NSFERASE,	ERINE P IKE FOLD	
PDB annotation	1 CARBON METABOLISM	TRANSFERASE SHMT, SERINE METHYLASE; ALPHA PLP ASPARTATE, AMINO TRANSFERASE, (AAT)-LIKE FOLD	TRANSFERASE SHMT; SERINE- GLYCINE CONVERSION, PYRIDOXAL 5-PHOSPHATE, 2 TETRAHYDROFOLATE, ASYMMETRIC DIMER.	TRANSFERASE TRANSFERASE, METABOLIC ROLE, PYRIDOXAL 5'- PHOSPHATE	AMINOTRANSFERASE PSAT; AMINOTRANSFERASE, L-SERINE BIOSYNTHESIS	AMINOTRANSFERASE PSAT; AMINOTRANSFERASE, L-SERINE BIOSYNTHESIS	TRANSFERASE PSAT; AMINOTRANSFERASE, PYRIDOXAL-S-PHOSPHATE, PHOSPHOSRINE, 2 AI KAI IPHILIC	LYASE ALPHA/BETA FOLD	TRANSFERASE SHMT; HYDROXYMETHYL TRANSFERASE, I CARBON METABOLISM	TRANSFERASE SHMT, SERINE METHYLASE, ALPHA PLP ASPARTATE, AMINO TRANSFERASE, (AAT)-LIKE FOLD	an order of the case of the case of the
Coumpound	ASE; CHAIN: A, B;	SERINE HYDROXYMETHYLTRANSFER ASE; CHAIN: A, B, C, D;	SERIND HYDROXYMETHYLTRANSFER ASE; CHAIN: A, B, C, D;	SERINE HYDROXYMETHYLTRANSFER ASE; CHAIN: A;	PHOSPHOSERINE AMINOTRANSFERASE; CHAIN: A. B:	PHOSPHOSERINE AMINOTRANSFERASE; CHAIN: A. B.	PHOSPHOSERINE AMINOTRANSFERASE; CHAIN: A;	CSDB PROTEIN: CHAIN: A:	SERINE HYDROXYMETHYLTRANSFER ASE: CHAIN: A. B.	SERINE HYDROXYMETHYLTRANSFER ASE; CHAIN: A, B, C, D;	Committee and the committee of the commi
SEQFOL D score					282.66						
PMF		99'0	0.42	0.18		1.00	1.00	0.48	0.43	-0.02	200
Verify		0.11	-0.02	0.15		0.58	0.59	-0.01	-0.04	0.07	000
Psi Blast		1.7e-67	1.7e-66	3,4e-62	1.7e-49	1.7e-49	5.1e-51	8.5e-56	6.80-62	5.1c-66	61.50
END AA		386	386	344	343	337	336	344	344	344	244
STAR T AA		80		1	26	27	25	=		3	-
CHAI		¥	V V	A	A	V	∢	¥	¥.	∢ .	
EDB EL		Idfo	leji	1bj4	1bjn	1bjn	1bt4	1con	1ej0	dfb 1	loii
SEQ No de		1606	1606	1607	1607	1607	1607	1607	1607	1607	1607

		×	2		Ī	100	T
PDB annotation	PYRIDOXAL S'-PHOSPHATE, 2 TETRAHYDROFOLATE, ASYMMETRIC DIMER	COMPLEX (TRANSCRIPTION FACTORDAY, TRANSCRIPTION FACTOR, PROTEIN-DINA COMPLEX, CYTORINE 2 ACTIVATION COMPLEX (TRANSCRIPTION FACTOR/DNA)	CHAPERONE ARCHAEAL PROTEIN	CONTRACTILE PROTEIN TRIPLE- HELLX COILED COIL, CONTRACTILE PROTEIN		LIGASE CBL, UBCHY, ZAP-70, E2, UBIQUITM, E3, PHOSPHORYLATION, 2 TYROSINE KINASE, UBIQUITINATION, PROTEIN DEGRADATION,	TRANSFERASE RECEPTOR TYROSINE KINASE, PROTEIN INTERACTION MODULE, 2 DIMERIZATION DOMAIN, TRANSFERASE
Coumpound	ASE; CHAIN: A, B, C, D;	STAT3B; CHAIN: A; 18-MER DESOXYOLIGONUCLEOTIDE; CHAIN: B;	PREFOLDIN; CHAIN: A; PREFOLDIN; CHAIN: B; PREFOLDIN; CHAIN: C;	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	VIRUS EQUINE HERPES VIRUS- 1 (C3HC4, OR RING DOMAIN) 1 CHC 3 (NMR, 1 STRUCTURE) 1 CHC 4	SIGNAL TRANSDUCTION PROTEIN CBL, CHAIN: A; ZAP. 70 PEPTIDE, CHAIN: B; UBIQUITIN-CONUGATING ENZYME E12-18 KDA UBCH?; CHAIN: C,	EPHAA RECEPTOR TYROSINE KINASE; CHAIN: A;
SEQFOL D score				70.36			
PMF		0.04	0.11		0.01	0.22	0.04
Verify score		-0.48	-0.33		-0.23	-0.31	0.02
Psi Blast		0.00051	1.2e-06	7.5e-05	3.4e-11	0.003	6.8e-14
END		0.2	82	345	903	611	885
STAR T AA		_	-	96	552	515	828
CHAI N ID		Ą	٧	V V		∢	e e
EDB LD		Ibg1	Ifxk	Iquu	Iche	Ifbv	1b0x
SEQ No B		1608	1608	1609	1612	1612	1614

		1	1	I				_
PDB annotation	SIGNAL TRANSDUCTION SAM DOMAIN, EPH RECEPTOR, SIGNAL TRANSDUCTION, OLIGOMER	CALCIUM-BINDING PROTEIN CALB; CALCIUM-+PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM- BINDING PROTEIN	CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM- BINDING PROTEIN	CALCTUM-BINDING PROTEIN CALB; CALCTUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCTUM- BINDING PROTEIN	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, BYDOCYTOSIS/EXOCYTOSIS	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, BYDOCYTOSIS/EXOCYTOSIS	LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID
Coumpound	EPHB2; CHAIN: A, B, C, D, E, F, G, H;	PROTEIN XINASE C (BETA); CHAIN: A, B;	PROTEIN KINASE C (BETA); CHAIN: A, B;	PROTEIN KINASE C (BETA); CHAIN: A, B;	SYNAPTOTAGMIN I; CHAIN: A;	SYNAPTOTAGMIN I; CHAIN: A;	SYNAPTOTAGMIN I; CHAIN: A;	PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;
SEQFOL D score								
PMF	-0.09	1.00	1.00	0.37	1.00	0.59	0.89	0.00
Verify score	0.21	0.08	0.32	0.33	-0.05	-0.02	0.85	-0.50
Psi Blast	6.8e-15	1.5e-26	4.5e-16	1.5e-36	3e-28	1.2e-08	6.8e-22	1.5e-14
END	885	716	864	871	7117	721	856	669
STAR T AA	825	588	728	755	588	819	732	909
CHAI N ID	4	4	∢	<	∢	¥	∢	A
PDB ID	1b4f	1a25	1a25	1a25	Ibyn	lbyn	Ibyn	Idjx
SEQ NO.	1614	1616	1616	9191	1616	1616	1616	9191

Verify PMF SEQPOL.
1.00 SYNAPTOTAGMIN III; CHAIN: A;
1.00 PROTEIN KINASE C, ALPHA TYPB; CHAIN: A;
0.99 PROTEIN KINASE C, ALPHA TYPE, CHAIN: A;
0.17 PROTEIN KINASE C, ALPHA TYPE, CHAIN: A;
0.58 PHOSPHOLIPASE A2; CHAIN: NULL;
1.00 CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAAPTOTAGMINI (FRST C2 DOMAIN! (CALB) 1R85 73
0.59 CALCIUMPHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3
0.36 RABPHILIN 3-A; CHAIN: A;

PDB annotation	DOMAINS, C2B-DOMAIN, RABPHILIN, ENDOCYTOSIS/EXOCYTOSIS	CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM- BINDING PROTEIN	CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM- BINDING PROTEIN	CALCIUM-BINDING PROTEIN CALB;	CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM- BINDING PROTEIN	ENDOCYTOSIS/EXOCYTOSIS	SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS,	NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS	ENDOCYTOSIS/EXOCYTOSIS	SYNAPTOTAGMIN, CZ-DOMAIN, EXOCYTOSIS,	NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS	ENDOCYTOSIS/EXOCYTOSIS	SYNAPTOTAGMIN, CZ-DOMAIN, EXOCYTOSIS.	NEUROTRANSMITTER 2 RELEASE,	HYDROLASE CPLA2; PHOSPHOLIPASE, LIPID-BINDING, HYDROLASE
Coumpound		PROTEIN KINASE C (BETA); CHAIN: A, B;	PROTEIN KINASE C (BETA); CHAIN: A, B;	PROTEIN KINASE C (BETA);	CHAIN: A, B;	SYNAPTOTAGMIN I; CHAIN: A;			SYNAPTOTAGMIN I; CHAIN: A;			SYNAPTOTAGMIN I; CHAIN: A;			CYTOSOLIC PHOSPHOLIPASE A2; CHAIN: A, B;
SEQFOL D score				59.65											
PMF		0.34	1.00			0.21			1.00			00.1		,	-0.05
Verify		0.28	0.08			0.26			0.33			-0.05			0.13
Psi Blast		6.8e-27	1.5e-26	1.5e-26		6.8c-23			1.7e-27			3e-28			1.7e-16
END		351	197	208		343			961			198			333
STAR T AA		230	69	69		221			69			69			230
CHAI N ID		¥	A	V		Ą			٧			V			V V
PDB ID		1a2.5	Ia25	1a25		Ibyn			1byn			1byn			lejy
SEQ ON ON		1617	1617	1617		1617			1617			1617			1617

Coumpound PDB annotation		SYNAPTOTAGMIN III; CHAIN: ENDOCYTOSIS/EXOCYTOSIS BETA SANDWICH, CALCIUM ION, C2 DOMAIN	ROTEN KINASE C, ALPHA TRANSTERAGE CALCUMAT-1 TYPE, CHAIN: A, PHOSPHOLIPD BINDING PROTEIN, CALCULM-BINDING 2 PROTEIN, PROSPHATIDYL SERINE, PROTEIN KINASE C.	PROTEIN UNASE C, ALPHA TRANSFRASE CALCUM++ TYPE, CHAIN, A; CALCUM-BINDING 7 FROTEIN, PHOSPHATING 7. FROTEIN FROSPHATING 7 FROTEIN KINASE C	PROTEIN KINASE C, ALPHA TRANSTERASE CALCIUM+1- TYPE, CHAIR-A, CALCIUM-BINDING PROTEIN, PHOSPHOLIPD DINDING PROTEIN PHOSPHATIPY LSERINE, PROTEIN KINASE C	PHOSPHOLIPASE A2; CHAIN: HYDROLASE CALB DOMAIN, CALB HYDROLASE, C2 DOMAIN, CALB DOMAIN	CALCIUMPHOSPHOLIPID BINDING PROTEIN SYNAPTORGMIN (FIRST C2 DOMARIN) (CALD) RSY 3	CALCUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTORAGIN I (FIRST C2 DOMARIN (CALB) RSY 3	CALCIUM/PHOSPHOLIPID BINDING PROTEIN BINDING PROTEIN PROTEIN CALON STOCK	- A - K - A - A - A - A - A - A - A - A
	D score	SYNAPTO] A;	PROTEIN KINASI TYPE; CHAIN: A;	PROTEIN KINASI TYPE; CHAIN: A;	PROTEIN KINASE TYPE; CHAIN: A;	PHOSPHOI NULL;	CALCIUMPHOSPH BINDING PROTEIN SYNAPTOTAGMIN DOMAIN) (CALB) 11		CALCIUM/PHOSPH BINDING PROTEIN SYNAPTOTAGMIN POMARN (CAIR) I	
	score D:							69.42		
-	_	0.39	0.13	0.70	1.00	0.58	0.07		1.00	
Verify	score	-0.26	0.24	-0.23	-0.11	-0.09	0.16		0.39	
Psi Blast		3.4e-52	1.2e-28	3.4e-21	1.2e-27	9e-20	6.8e-23	6e-30	1.7e-27	
END	V	356	351	203	197	207	343	200	961	
STAR	V.	71	232	89	69	87	221	29	69	
CHAI	a v	∢	<	<	∢					
EDE	9	Idqv	Idsy	ldsy	ldsy	Irlw	Irsy	Irsy	Irsy	
SEQ	ξ	1617	1617	1617	1912	1617	191	1617	1617	

PDB annotation		ENDOCYTOSIS/EXOCYTOSIS C2- DOMANINS, C2B-DOMAIN, RABPHILIN, ENDOCYTOSIS/EXOCYTOSIS	ENDOCYTOSIS/EXOCYTOSIS C2-DOMAINS, C2B-DOMAIN, RABPHILIN, ENDOCYTOSIS/EXOCYTOSIS	ENDOCYTOSISEXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSISEXOCYTOSIS	TRANSFERASE CALCIUM++, PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYLSERINE, PROTEIN KINASE C		POTASSIUM CHANNELS POTASSIUM CHANNELS, TETRAMERIZATION DOMAIN, X- RAY 2 STRUCTURE, APL YSIA KVI.1	GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2
Coumpound	BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	RABPHILIN 3-A; CHAIN: A;	RABPHILIN 3-4; CHAIN: A;	SYNAPTOTAGMIN I; CHAIN: A;	PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	CALCIUMPHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN (PIRST C2 DOMAIN) (CALB) 1RSY 3	POTASSIUM CHANNEL KVI.1; CHAIN: NULL;	PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;
SEQFOL D score								
PMF		0.45	96.0	0.17	0.13	0.16	1.00	0.65
Verify		0.15	0.22	0.29	-0.00	0.14	0.38	0.65
Psi Blast		3.4e-27	8.5e-20	1.3e-06	0.0045	1.5e-05	5.1e-26	6.8e-05
END		354	206	366	356	366	&	104
STAR T AA		236	71	264	264	264	e e	5
CHA1 N ID		¥	A	4	∢			V
PDB		3rpb	3rpb	Ibyn	ldsy	Irsy	1a68	1buo
S a S		1617	1617	8191	1618	1618	1620	1620

PDB annotation	REPRESSOR, ZINC-FINGER PROTEIN, X-RAY CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION	SIGNALING PROTEIN VOLTAGE- GATED POTASSIUM CHANNEL, ASSEMBLY DOMAIN, TETRAMER		SIGNALING PROTEIN VOLTAGE. GATED POTASRUM CHANNEL, TETRAMERIZATION DOMAIN, 2 INTRACELLULAR GATE, TETRAMER.	PROTON TRANSPORT POTASSIUM CHANNELS, TETRAMERIZATION DOMAIN, X:RAY STRUCTURE, 2 APLYSIA KVI.1, PROTON TRANSPORT	POTASSIUM CHANNEL POTASSIUM CHANNEL, TETRAMERIZATION DOMAIN, MOLECULAR 2 RECOGNITION, ZINC-BINDING	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2.2 TANDEM 3-HELIX COLED-COLLS, STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2.2
Coumpound		KV1.2 VOLTAGE-GATED POTASSIUM CHANNEL; CHAIN: A, B, C, D, E, F, G, H;	KV BETA2 PROTEIN; CHAIN: A; POTASSIUM CHANNEL KV1.1; CHAIN: E;	KVI.2 VOLTAGE-GATED POTASSIUM CHANNEL; CHAIN: A, B, C, D;	POTASSIUM CHANNEL KV1.1; CHAIN: A;	POTASSIUM CHANNEL PROTEIN SHAW; CHAIN: NULL;	ALPHA SPECTRIN; CHAIN: A, B, C;	ALPHA SPECTRIN; CHAIN: A, B, C;
SEQFOL D score								53.11
PMF		66.0	0.99	0.82	0.95	1.00	0:01	
Verify score		0.28	0.31	-0.10	0.38	0.55	-0.18	
Psi Blast		3.4e-25	1.5e-26	1.7e-26	1.2e-26	8.5e-29	0.003	0.003
END		68	35	101	101	102	158	212
STAR T AA		6	2	er.	6	2	17	_
CHAI		Ą	В	∀	¥		۷.	∢.
PDB ID		1dsx	1exb	Iqdv	ри	3kvt	lcun	lcun
SEQ No: D		1620	1620	1620	1620	1620	1621	1621

PDB annotation	TANDEM 3-HELIX COLLED-COLLS, STRUCTURAL PROTEIN	CELL CYCLE REGULATION CELL CYCLE REGULATION, HERPESVIRUS SAIMIRI, VIRAL CYCLIN	CELL DIVISION RCYCLIN H (RECOMBINANT); CYCLIN, CELL CYCLE, CELL DIVISION, NUCLEAR PROTEIN	COMPLEX (PROTEIN RINASSUCALIN) CVCINI- BDERUDENT KINASES, CINGL, PS PROTEIN KINASES, CCNA, CCNI; COMPLEX (PROTEIN KINASE) CCNA, CCNI; RINASECYCLIN, CYCLIN, CDK, 2 PHONPHORY LATION, SUBSTRATE	COMPLEA BINDING PROTEIN CYCLIN, CELL CYCLE, KINASE-REGULATORY. SUBUNIT, 2 BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING
Coumpound		CYCLIN HOMOLOG; CHAIN: A;	CYCLIN H; CHAIN; NULL;	CELL DIVISION PROTEIN KINASB 2; CHANI'S, C; GZAMITOTIC-SPECIFIC CYCLIN A; CHAIN: B, D; SUBSTRATE PEPTIDE; CHAIN: E, F;	CYCLIN A; CHAIN: NULL;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE: CHAIN: B. C.	OGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING
SEQFOL D score								
PMF score		0.37	0.30	0.76	0.77	0.84	68.0	0.70
Verify score		0.02	0.03	0.33	0.40	0.35	-0.10	-0.01
Psi Blast		1.4e-19	1.2e-12	8.5e-42	1.7e-40	1.26-19	6.8e-22	1.4e-25
END		149	148	88	148	169	134	165
STAR T AA		52	78	14	47	110	33	70
CHAI		<		m		4	<	V
PDB TD		1bu2	Ijkw	Iqmz	Ivin	lalh	lalh	lalh
SEQ NO ESQ		1623	1623	1623	1623	1624	1624	1624

Coumpound PDB annotation		B, D, E; COMPLEX (ZINC FINGER/DNA) ZINC FINGER FINGER, PROTEIN-DNA		CRYSTAL STRUCTURE, COMPLEX				_				CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	Ī			(ZINC FINGER/DNA)	F			CRYSTAL STRUCTURE, COMPLEX		_				CRYSTAL STRUCTURE, COMPLEX	
ore	SITE; CHAIN: B, C;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;		DNA: CHAIN: A B D B.	CONSENSIIS ZINC FINGER	PROTEIN; CHAIN: C, F, G;		DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			_	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;	,	DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;	_	_	
SEQFOL D score					1		_			_	_	_		58.17				_									_	-
PMF		0.92			900	9			0.75									0.18					0.98					
Verify		0.35			-0.20	-0.23			90.0									-0.00					80.0					
Psi Blast		3.4e-33			1 70.41	į.			3.4e-45					3.4e-45				6.8e-38					1.5e-13					
END AA		169			134	<u> </u>			165					991				93					134				_	ŀ
STAR T AA		601			33	3			89					89				7					107				_	
CHAI N ID		o o			ن	ر			ပ					٥.				O					0					
PDB ID		Imey			Impo	, illing			1mey					Imey				lmey					lmey					
SEQ NO:		1624			1624	1021			1624					1624				1624				_	1624					

									_							_		_				
PDB annotation	CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIIIA; 5S GENE, NMR, THIIA; PROTEN, DNA,	JACANSCRATION FACIOR, 33 KNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION THERII ATTON/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) THIIA; 5S	GENE; NMR, TFIIIA, PROTEIN, DNA,	GENE, DNA BINDING PROTEIN,	ZINC FINGER, COMPLEX 3	(IKANSCKIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-YANG 1;	TRANSCRIPTION INITIATION,	INITIATION ELEMENT, 111, ZINC 2	PECOCNITION 2 COMMITTEE	ALCOGNITION, 5 COMPLEX	REGIL ATION/DIA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-YANG 1;	TRANSCRIPTION INITIATION,	INITIATOR ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-PROTEIN	KECOGNITION, 5 COMPLEX	(INAINSCRIPTION REGULATION/DNA)
Coumpound		TRANSCRIPTION FACTOR IIIA; CHAIN: A; SS RNA GENE; CHAIN: E, F;		TRANSCRIPTION FACTOR IIIA; CHAIN: A; 5S RNA GENE;	CHAIN: E, F;				YYI; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CEAIN: A, B;				YYI; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;			
SEQFOL D score																51.82						
PMF		0.12		0.25					-0.02													
Verify		0.43		-0.23					0.21													
Psi Blast		Ie-14		3.4e-17					I.7e-13							5.1e-28						
END AA		691		165					691							991						
STAR T AA		110		69					117							30						
CHAI		¥.		¥					υ							O						
10 E		EHI		EEE					Iubd							lubd						
SEQ NO D		1624		1624			•		1624					_		1624						
						731																

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PDB annotation	COMPLEX (TRANSCRIPTION REGULATION/DNI) YING-YANG I; RRANSCRIPTION INTIATION, INITIATION, INITIATION, INITIATION, INITIATION, EPICHER RECOGNITION, 3 COMPLEX (TRANSCRIPTION). 3 COMPLEX (TRANSCRIPTION). 3 ENGULATION/DNA).	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADRI, ZINC FINGER, NMR		COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	OXIDOREDUCTASE PDZ DOMAIN, NNOS, NITRIC OXIDE SYNTHASE	OXIDOREDUCTASE PDZ DOMAÏN, NNOS, NITRIC OXIDE SYNTHASE	PEPTIDE RECOGNITION PEPTIDE RECOGNITION, PROTEIN
Coumpound	YYI; CHAIN: C; ADBNO- SROCIATED VIRUS P\$ INITIATOR ELEMENT DIA; CHAIN: A, B;	ADRI; CHAIN: NULL;	COMPLEX(TRANSCRIPTION REGULATION/DNA) TRAMTRACK PROTEIN (TWO ZINC-FINGER PEPTIDE) COMPLEXED WITH 2DRP 3 DNA 2DRP 4	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	NEURONAL NITRIC OXIDE SYNTHASE; CHAIN: A; HEPTAPEPTIDE; CHAIN: B;	NEURONAL NITRIC OXIDE SYNTHASE; CHAIN: A; HEPTAPEPTIDE; CHAIN: B;	PSD-95; CHAIN: A; CRIPT; CHAIN: B;
SEQFOL D score						54.14		52.53
PMF	0.42	0.63	0.29	0.10	0.09		0.84	
Verify score	-0.13	-0.20	0.14	0.03	0.01		0.83	
Psi Blast	5.1e-28	3.40-15	1e-09	6.8e-25	8.5e-21	4.56-19	4.50-19	1.5e-14
END	165	167	165	164	169	186	181	170
STAR T AA	39	110	105	13	16	95	99	48
CHAI	υ		∢	∢	4	A	V	V
PDB CI	Iubd	2adr	2drp	2gli	2gti	1b8q	Ib8q	lbe9
SEQ No.	1624	1624	1624	1624	1624	1627	1627	1627

PDB annotation	LOCALIZATION	PEPTIDE RECOGNITION PEPTIDE RECOGNITION, PROTEIN LOCALIZATION	CYTOKINE LCF; CYTOKINE, LYMPHOCYTE CHEMOATRACTANT FACTOR, PDZ DOMAIN	CYTOKINE LCF; CYTOKINE, LYMPHOCYTE CHEMOATTRACTANT FACTOR, PDZ DOMAIN	KINASE HCASK, GLGF REPEAT, DHR; PDZ DOMAIN, NEUREXIN, SYNDECAN, RECEPTOR CLUSTERING, KINASE	OXIDOREDUCTASE BETA-FINGER	MEMBRANE PROTEINOXIDOREDUCTASE BETA- FINGER, HETERODIMER	PEPTIDE RECOGNITION PSD-95; PDZ DOMAIN, NEURONAL NITRIC OXIDE SYNTHASE, NMDA RECEPTOR 2 BINDING	PEPTIDE RECOGNITION PSD-95; PDZ DOMAIN, NEURONAL NITRIC OXIDE SYNTHASE, NMDA RECEPTOR 2 BINDING	HYDROLASE PDZ DOMAIN, HUMAN PHOSPHATASE, HPTP1E, PTP-BAS,
Coumpound		PSD-95; CHAIN: A; CRIPT; CHAIN: B;	INTERLEUKIN 16; CHAIN: NULL;	INTERLEUKIN 16; CHAIN: NULL;	HCASK/LIN-2 PROTEIN; CHAIN: A, B;	NEURONAL NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: A;	ALPHA-1 SYNTROPHIN (RESIDUES 77-171); CHAIN: A; NEURONAL NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: B;	POSTSYNAPTIC DENSITY PROTEIN 95; CHAIN: A;	POSTSYNAPTIC DENSITY PROTEIN 95; CHAIN: A;	TYROSINE PHOSPHATASE (PTP-BAS, TYPE 1); CHAIN: A;
SEQFOL D score			70.34							
PMF		0.24		0.76	86:0	0.37	1.00	1.00	0.17	0.65
Verify		0.12		0.39	0.55	0.47	1.02	0.75	0.05	0.30
Psi Blast		1.50-14	3e-22	3e-22	3e-19	1.2e-20	6e-20	3e-22	1.5e-15	1.7e-17
END		153	191	157	149	176	149	149	143	143
STAR T AA		86	35	19	19	29	1.9	19	\$8	26
CHAI N ID		٧			V	<	٧	A	A	٧
PDB ID		lbe9	1116	1116	1kwa	Iqau	lqav ^	lqlc	1qlc	3pdz
SEQ No.		1627	1627	1627	1627	1627	1627	1627	1627	1627

	_				_	-			_			_			_			_	_				
PDB annotation	SPECIFICITY 2 OF BINDING	HYDROLASE PDZ DOMAIN, HUMAN PHOSPHATASE, HYPPIE, PTP-BAS, SPECIFICITY 2 OF BINDING	LIPID TRANSPORT APO A-1; LI-DOPROTEIN, LIPID TRANSPORT, CHOLESTEROL METABOLISM, 2 ATHEROSCLEROSIS, HDI, LCAT- ACTIVATION	DESIGNED HELICAL BUNDLE DESIGNED HELICAL BUNDLE		RNA-BINDING PROTEIN/RNA TRA	REGULATION, RNP DOMAIN, RNA	COMPLEX	RNA-BINDING PROTEIN/RNA TRA	PRE-MRNA; SPLICING	KEGULA HUN, KNF DOMAIN, KNA COMPLEX	RNA-BINDING PROTEIN/RNA TRA	PRE-MRNA; SPLICING	REGULATION, RNP DOMAIN, RNA	COMPLEX	GENE REGULATION/RNA POLY(A)	BINDING PROTEIN 1, PABP 1; RRM,	PROJEIN-RNA COMPLEX, GENE	KEGULA HUNKINA		GENE REGULATION/RNA POLY(A)	BINDING PROTEIN 1, PABP 1; RRM,	PROTEIN-RNA COMPLEX, GENE
Coumpound		TYROSINE PHOSPHATASE (PTP-BAS, TYPE 1); CHAIN: A;	APOLIPOPROTEIN A-1; CHAIN: A, B, C, D;	DHP1; CHAIN: NULL;		SXL-LETHAL PROTEIN; CHAIN:	R(P*GP*UP*UP*UP*UP*	UP*UP*UP*UP*U)- CHAIN: P, Q;	SXL-LETHAL PROTEIN; CHAIN:	A, B; KNA (5'-	UP* UP* UP* UP* UP* UP. CHAIN: P, Q;	SXL-LETHAL PROTEIN; CHAIN:	A, B; RNA (5'-	R(P*GP*UP*UP*UP*UP*	UP*UP*UP*UP*U)- CHAIN: P, Q;	POLYDENYLATE BINDING	PROTEIN I; CHAIN: A, B, C, D,	E, F, G, H; KNA (5" DOSADSADSADSADSADSADS	Ans and an an an an an an an	O. P. O. R. S. T.	POLYDENYLATE BINDING	PROTEIN 1; CHAIN: A, B, C, D,	E, F, G, H, KINA (3-
SEQFOL D score			63.32						74.65												81.71		
PMF		1.00		0.01		0.78						1.00				00.							
Verify		0.92		0.12		0.78						0.91				96.0							_
Psi Blast		4.5e-22	5.1e-07	0.0043		1.7e-16			1.5e-36			1.5e-36			00 1 0	3.4e-20					1.7e-34		
END		149	258	366		128			231			229			0,1	148					237		
STAR		56	53	325		51			89			100				280					70		
CHAI N ID		٧	¥			Ą			٧			Ą				۷					۷		
E GI		3pdz	lav1	4hb1		167f			167£			1b7f				lovj					1cvj		
SEQ NO:		1627	1628	1628		1629			1629			1629			00/1	1629					1629		

rd PDB annotation	"P*AP*AP* REGULATION/RNA AAIN: M, N,	NDING GENE REGULATIONRNA POLY(A) A, B, C, D, BINNOG PROTENT, PARP 1; RRM, PROTEIN-RAA, COMPLEX, GENE PROTEIN-RAA, COMPLEX, GENE ARN: M, N, HEGULATIONRNA	NDING GENE REGULATION/RNA POLY(A) A, B, C, D, BINDING PROTEIN I, PABP I; RRM, PROTEIN-RNA COMPLEX, GENE P*AP*AP* REGULATION/RNA HAIR: M, N,	NDING A. B. C, D. BINDING PROTEIN: I, PABP 1; RRM, PPAP* AP* PROTEIN-RNA COMPLEX, GENE PROTEIN: M, N, REQULATION/RNA	NDING A, B, C, D, BINDING PROTEIN I, PABP I, SRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA HARP, M, N,	MDING GENE REGULATION/RNA POLY(A) A. B. C. D. RINDING PROTEIN I, PABP I; RRM, PROTEIN-RNA COMPLEX, GENE PEAP-AP-AP REGULATION/RNA A.N. M. N.
Coumpound	R(*AP*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*A); CHAIN: M, N, O. P. O. R. S. T.	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5*, R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*	POLYDENYLATE BINDING PROFIEN I; GHANI'S, B, C, D, E, F, G, H; RIM (5'- R(*Al*Al*Al*Al*Al*Al*Al*Al* Al*Al*Al*Al*Al*Al* O, P, C, R, S, T;	POLYDENYLATE BINDING PROOFEN!; CHANI: A, B, C, D, E, F, G, H; RNA (5'- R(*Al*Al*Al*Al*Al*Al*Al*Al* Al*Al*Al*Al*Al*Al*Al* Al*Al*Al*Al*Al*Al* O, P, Q, R, S, T;	POLYDENYLATE BINDING PROFIEN I; CHANFI: A,B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP* AP*AP*AP*AP*AP* AP*AP*AP*AP*AP* O, P, O, R, S, T, S); CHAIN: M, N,	POLYDENYLATE BINDING PROTEIN 1: CHANN: A, B, C, D, E, F, G, H, RNA (5'- R(*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP*AN: M, N,
SEQFOL D score			75.65		52.68	
PMF		00.1		8.1		1.00
Verify score		0.89		0.71		0.41
Psi Blast		1.7e-34	1e-30	1e-30	le-33	5.1e-27
END		233	218	202	212	202
STAR		17	07	71	70	7.1
CHAI		<	æ	м	ĬĽ.	Ţri
PDB ID		levj	lovj	lcvj	lcvj	lovj
SEQ ID	ÖN	1629	1629	1629	1629	1629

PCT/US02/05095

PDB annotation	BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	GENE REGULATIONRNA POLY(A) BINDING RECTEN I, PARP I, RRM, PROTEIN-RAA COMPLEX, GENE REGULATIONRNA	GENE REGULATION/RNA POLY(A) BINDING PROTEIN I, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	GENE REGULATIONRNA POLY(A) BINDING PROTEIN I, PABP 1; RRM, PROTEIN-NA COMPLEX, GENE REGULATIONRNA	NUCLEAR PROTEIN HETEROGRAPIOUS NUCLEAR HETEROGRAPIOUS NUCLEAR HROWUCLEAR PROTEIN, HINRYP, RBD, RUCLEAR PROTEIN, HINRYP, RBD, RRWA, RNP, RNA BINDING, 2 RBOWUCLEOPROTEIN	NUCLEAR PROTEIN HETEROGENBOUS NUCLEAR KIBONUCLEOPROTEIN A1, NUCLEOR PROTEIN, HNRNP, RBD, RRM, RNF, RNA BINDING, 2
Coumpound	PROTEIN I; CHAIN: A, B, C, D, PR PR E, F, G, H; RNA (5* R(*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP; CHAIN: M, N, O, P, Q, F, S, T.	TE BINDING AIN: A, B, C, D, (5'- AP*AP*AP*AP* 3'); CHAIN: M, N,	IE BINDING AIN: A, B, C, D, (5'- AP*AP*AP*AP* 3'); CHAIN: M, N,	POLYDENYLATE BINDING GI PROTEIN I, CHAMIA, B, C, D, BE, F, G, H; RNA (S. R(*AP*AP*AP*AP*AP*AP*AP* R(*AP*AP*AP*A); CHAIN; M, N, O, P, Q, R, S, T;	ADN: NULL;	HNRNP A1; CHAIN: NULL; HI HI RI
SEQFOL D score		53.52				
PMF			0.10	0.99	00.1	1.00
Verify			0.35	0.51	0.69	1.05
Psi Blast		1.4e-31	8.5e-27	1.46-31	3.46-25	3.46-56
END		509	202	209	44	229
STAR T AA		70	11	72	52	છ
CHAI		I	ш	н		
PDB		1cvj	1cvj	levj	lha1	Ihal
SEQ No es		1629	1629	1629	1629	1629

PDB CHAI STAR END Fsi Blast Verify ID NID TAA AA score Ibal 66 230 3.46-36	CHAI STAR END Psi Blast NID TAA AA	STAR END Psi Blast TAA AA STAR AA STAR AA STAR STAR	AA Psi Blast AA 3.4e-56	AA Psi Blast AA 3.4e-56	Psi Blast 3.4e-56	Verify		PMF	SEQFOL D score	Coumpound HNRNP A1; CHAIN: NULL;	PDB annotation RIBONUCLEOPROTEIN NUCLEAR RROTBIN HETER OGENEOJIS NICI JEAR
A 71 144 3.4e.27 1.26	71 144 3.4e.27 1.26	144 3.4e-27 1.26	144 3.4e-27 1.26	3.4e-27 1.26	1.26			1.00		HETEROGENBOUS NUCLEAR RIBONUCLEOPROTEIN DO; CHANN: A:	RIBONUCLEOPROTEIN 41, NUCLEAR PROTEIN HYRNP, RBD, RRM, RNP, RNA BINDING, 2 REBONUCLEOPROTEIN RNA BINDING PROTEIN RNA- BINDING DOMAIN
hdi A 71 145 1.5e-27 1.29	71 145 1.5e-27	145 1.5e-27	145 1.5e-27	1.5e-27		1.29		00:1		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN DO; CHAIN: A;	RNA BINDING PROTEIN RNA- BINDING DOMAIN
osm A 235 329 1.5e-11 1.27	235 329 1.5e-11	329 1.5e-11	329 1.5e-11	1.56-11	-	1.27		-0.19		OMPK36; CHAIN: A, B, C;	OUTER MEMBRANE PROTEIN OSMOPORIN; OUTER MEMBRANE PROTEIN, NON-SPECIFIC PORIN, OSMOPORIN; 2 BETA-BARREL, TRANSMEMBRANE
	241 324 1.5e-11	324 1.5e-11	324 1.5e-11	1.5e-11		1.08	-	-0.19		OUTER MEMBRANE PROTEIN PHOSPHOPORIN (PHOE) 1PHO 3	
qm9 A 22 145 6e-17 0.55	22 145 66-17	145 6e-17	145 6e-17	6e-17		0.55		0.23		POLYPYRIMIDINË TRACT- BINDING PROTEIN; CHAIN: A;	KIBONUCLEOPROTEIN PTB. PTB. C198, HETTBROGENBOU'S NUCLEAR POLYPYRIMIDINE TRACT BINDING PROTEIN, RNP, RNA, SPICING, 2 TRANSLATION
sxd 61 150 66-25 0.066	150 6e-25	150 6e-25	150 6e-25	6e-25		0.66		0.60		RIN-BRIDING PROTEIN SEX- LETHAL PROTEIN (C- TERARING), GR SECOND. RIN- BRIDING DOMANI I SXL. 3 (RBD-2), RESIDUES 199 - 294 PLUS N-FERMINAL MET) I SXL. 4 (PARR, 17 STRUCTURES) I SXL.	
sxl 62 150 1.7e-16 0.71	150 1.7e-16	150 1.7e-16	150 1.7e-16	1.7e-16	П	0.71	\vdash	0.45		RNA-BINDING PROTEIN SEX-	And the second s

PDB annotation		INTEGRAL MEMBRANE PROTEIN PORIN MATRIX PORIN, OMPF PORIN; 20MF 7 PORIN, MEMBRANE PROTEIN 20MF 12	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETIROGENEOUS UNCLEAR 2 RIBONUCLEOPROTEIN A1	COMPLEX (RIDONUCLEOPROTEIN/DNA) HINRIW A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETIROGENBOUS UUCLEAR 2 RIDONUCLEOPROTEIN A1	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETRROGENBOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3
Coumpound	LETHAL PROTEIN (C. TERMINUS, OR SECOND RNA- BINDING DOMAIN 1SXL 3 (RBD-2), RESIDUES 199 - 294 PLUS N-TERMINAL MET) 1SXL 4 (NMR, 17 STRUCTURES) 1SXL 3	MATRIX PORIN OUTER MEMBRANE PROTEIN F; 20MF 5 CHAIN: NULL; 20MF 6	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHANI: A: 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHANI: A: 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DIVA; CHAIN: B;	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHANI: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	SEX-LETHAL; CHAIN: A, B, C,
SEQFOL D score					165.44	70.15
PMF		-0.20	1.00	1.00		
Verify score		1.23	1.05	1.18		
Psi Blast		9e-13	1e-28	5.1e-57	5.1e-57	5.1e-36
END		328	144	233	239	229
STAR T AA		237	52	64	25	69
CHAI			∢	∢	⋖	<
EDB ED		20mf	2up1	2up1	2up1	3sxl
S a S		1629	1629	1629	1629	1629

			_		_			_	
PDB annotation	DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRN, 2 SPLICING INHBITOR, TRANSLATIONAL, THEIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION		COAGULATIONCRY YSTA1. STRUCTURE/HEFARIN-B FACTOR IIA; COAGULA-ITON/CRY YSTA1. STRUCTURE/HEFARIN-BINDING SITE/2 HIRUDIN/THROMBIN INHBITOR		CONTRACTILE PROTEIN MIXED ALPHA-BETA STRUCTURE, ACTIN- BINDING PROTEIN, PROTEIN 2 DOMAIN PACKING, CONTRACTILE PROTEIN	CONTRACTILE PROTEIN MIXED LEPHA-BERTA STRUCTURE, ACTIN- BINDING PROTEIN, PROTEIN 2 DOMANN PACKING, CONTRACTILE PROTEIN		OOMPLEX (TWO DNA-BINDING PROTEINS/DNA) MAT ALPHA-2; COMPLEX (TWO DNA-BINDING PROTEINS/DNA), COMPLEX, 2 DNA- BINDING PROTEIN, DNA, TRANSCRIPTION REGITA TION
Coumpound		SEX-LETHAL; CHAIN: A, B, C;		THROMBIN; CHAIN: A,B,C; THROMBIN; CHAIN: D,B,F; HAEMADIN; CHAIN: I,J,K;		HORSE PLASMA GELSOLIN; CHAIN: A, B	HORSE PLASMA GELSOLIN; CHAIN: A, B		MATING-TYPE PROTEIN A-1; CHAIN: A, MATING-TYPE PROTEIN ALPHA-2; CHAIN: B; DNA; CHAIN: C;
SEQFOL D score			-				876.96		
PMF		1.00		86:0		1.00			0.95
Verify score		0.88		0.77		0.81			0.54
Psi Blast		5.1e-36		0.006		0	0		90-99
END AA		229		48		715	715		130
STAR T AA		70		47		85	'n		8
CHAI		∢				¥	∢		∢
PDB TD		3sxl		le0f		1d0n	140n	1	lakh
SEQ NO ID		1629		1635		1637	1637		1641

PDB annotation	COMPLEX (DNA-BINDING PROTEINDING) GHF-I; COMPLEX (DNA-BINDING PROTEINDINA), PITUITARY, CPHD, 2 POU DOMAIN, TRANSCRIPTION FACTOR.	PROTEINDNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA	DNA-BINDING PROTEIN ISL-1HD DNA-BINDING PROTEIN, HOMEODOMAIN, LIM DOMAIN	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION		DNA-BINDING PROTEIN	
Coumpound	PIT-1; CHAIN: A, B; DNA; CHAIN: C, D;	HOMEOBOX PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E;	INSULIN GENE ENHANCER PROTEIN ISL-1; CHAIN: NULL;	PAIRED PROTEIN: CHAIN: A, B, C; DNA; CHAIN: D, E, F	PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	DNA-BINDING PROTEIN OCT-2 POU HOMEODOMAIN (NMR, AVERAGE STRUCTURE) 1HDP 3	OCT-3; 10CP 5 CHAIN: NULL; 10CP 6	TO AND AIR INDIVIDE REQUENT OF THE INDIVIDUAL POUT HOMEODOWALNI DNA. BINDING PROTEIN MUTANT WITH HOGS ARE GLY SER. HIS MET INSERTED AT THE BY. TERMINUS AND ASP LIE POOR AT THE CANNING AND ASP LIE POOR ASP
SEQFOL D score								
PMF	0.55	0.33	0.49	86.0	86.0	69:0	0.62	0.78
Verify score	0.22	-0.02	0.17	0.89	0.71	0.33	99.0	0.46
Psi Blast	7.5e-06	1.5e-05	1.5e-06	1.2e-05	9e-06	90-99	1.3e-06	36-06
END	134	136	134	134	134	134	134	134
STAR	32	25	92	35	92	83	25	83
CHAI	∢	ш		⋖	æ			
10 E	lau7	1672	1bw5	101	<u> </u>	1hdp	locp	godı
SEQ NO.	1641	1641	1641	1641	1641	1641	1641	1641

PDB annotation																											
Coumpound	13 STRUCTURES) IPOG 6	HYDROLASE(CARBOXYLIC ESTERASE) LIPASE (E.C.3.1.1.3) COMPLEXED WITH COLIPASE	AND INHIBITED ILPB 3 BY	METHYL ESTER (TWO CONFORMATIONS) 1LPB 4	HYDROLASE(CARBOXYLIC	ESTERASE) LIPASE (E.C.3.1.1.3)	COMPLEXED WITH COLIDASE AND INHIBITED II PR 3 BY	UNDECANE PHOSPHONATE	METHYL ESTER (TWO	CONFORMATIONS) ILPB 4	HYDROLASE(CARBOXYLIC	ESTERASE) LIPASE (E.C.3.1.1.3)	COMPLEXED WITH COLIFASE	AND INHIBITED ILPB 3 BY	ONDECAME PROSPHONALE	METHYL ESTER (TWO CONFORMATIONS) 1LPB 4	LIPASE PROTEIN COFACTOR	PORCINE PANCREATIC	PROCOLIPASE B IPCN 3 (NMR,	MINIMIZED AVERAGE	STRUCTURE) IPCN 4	LIPASE PROTEIN COFACTOR	PORCINE PANCREATIC	PROCOLIPASE B IPCN 3 (NMR,	MINIMIZED AVERAGE	SIRUCIORE) IPCN 4	LIPASE PROTEIN COFACTOR
SEQFOL D score											50.95																26.60
PMF		0.81			88.0												1.00					1.00					
Verify score		-0.36			-0.35												-0.36					-0.36				Ī	
Psi Blast		8e-19			3e-20						3e-20						3.2e-20					6e-22				00	77-20
END		4			59						9						69					69				5	66
STAR		53			29												29					29					-1
CHAI N ID		∢			4						A																
FDB ID		1lpb			11pb						Ilpb						lpcn					Ibcu			_		1 Don
Se d Se		1653			I653						1653						1653					1653				1687	1000

PDB annotation		COMPLEX (TRANSFERASE/PEPTIDE) COMPLEX (TRANSFERASE/PEPTIDE)	V-SRC SH2 DOMAIN SRC SH2; V- SRC SH2 DOMAIN, PHOSPHOTYROSINE RECOGNITION DOMAIN, PP60 2 SRC SH2 DOMAIN	PHOSPHORYLATION SIGNAL TRANSDUCTION, TYROSINE KINASE, TRANSFERASE, 2 PHOSPHORYLATION PHOSPHORYLATION	SIGNALING PROTEINTRANSFERASE NAK; COMPLEX, SIGNAL TRANSDUCTION; PHOSPHOTYROSINE BINDING 2 DOMARIN (PTB), ASYMMETRIC CELL DIVISION	PHOSPHOTRANSFERASE C-SRC, PROSPICATION SER, TYRONSE KINASE, PHOSPHORY I.A. (TION, SEP, SEP, 2 PHOSPHOTYROSINE, PROTO- ONCOCERE, PHOSPHOTRANSFRASE	
Coumpound	PORCINE PANCREATIC PROCOLIPASE B IPCN 3 (NMR, MINIMIZED AVERAGE STRUCTURE) IPCN 4	C-SRC TYROSINE KINASE; CHARI: A, B, ACE-FORMYL PHOSPHOTYR-GLU-(N,N- DIPENTYL AMINE); CHAIN: C, D:	PF60 V-SRC TYROSINE KINASE TRANSFORMING PROTEIN; CHAIN: NULL;	P55 BLK PROTEIN TYROSINE KINASE; CHAIN: NULL;	NUMB PROTEIN; CHAIN: A; NUMB ASSOCIATE KINASE; CHAIN: B;	TYROSINE-PROTEIN KINASE SRC; CHAIN: NULL;	PHOSPHOTRANSFERASE V- SRC TYROSINE KINASE
SEQFOL D score							
PMF		0.03	90.00	0.11	0.95	0.01	0.04
Verify score		-0.10	-0.06	-0.37	80.0	-0.32	-0.17
Psi Blast		3.2e-28	3.2e-29	3.2e-27	3e-17	3.2e-44	9.6e-29
END		66	102	8	247	165	66
STAR T AA	-	_	-	_	120	-	_
CHAI		<			¥		¥
EDB TD		1a09	Ibki	161	1ddm	1fmk	Isha
SEQ Sign		1654	1654	1654	1654	1654	1654

PDB annotation		COMPLEX (SIGNAL TRANSDUCTION/PETIDE) COMPLEX (SIGNAL TRANSDUCTION/PETIDE), PHOSPHOTYROSINE 2 BINDING DOMAIN (PTB)	CELL, CYCLEGEN REGULATION COMPLEX, SIGNAL TRANSDUCTION, PHOSPHOTYROSINE BINDING 2 DOMAIN (PTB), ASYMETR IC CELL DIVISION, CELL CYCLEGENE 3 REGILATION	CELL CYCLE/GENE REGULATION COMPLEX, SIGNAL TRANSDUCTION, PHOSPHOTYROSINE BINDING 2 DOAMN (FTB), ASYMETR IC CELL DIVISION, CELL CYCLE/GENE 3 REGULATION	CELL CYCLEGENE REGULATION COMPLEX, SIGNAL TRANSDUCTION, PHOSPHOTYROSINE BINDING 2 DOMAIN (PTB), ASYMETR IC CELL DIVISION, CELL CYCLEGENE 3
Coumpound	(PHANSEORMING PROTEIN (PHANSEORMING ISHA) RECOGNITION DOMAIN SED (CATALLIE) COMPEEX WITH ISHA 4 PHOSPHOPEPTIDE A (TYR-VAL-PRO-MET-LEU, PHOSPHORYLATED TYR) ISHA	SHC: CIAIN: A; TRKA RECEPTOR PHOSPHOPEPTIDE; CHAIN: B;	NUMB PROTEIN; CHAIN: A; GPPY PEPTIDE; CHAIN: B;	NUMB PROTEIN; CHAIN: A; GPPY PEPTIDE; CHAIN: B;	NUMB PROTEIN; CHAIN: A; GPPY PEPTIDE; CHAIN: B;
SEQFOL D score				51.48	
PMF		0.10	0.93		86'0
Verify score		0.17	0.21		0.34
Psi Blast		0.00075	9e-24	96-24	0.00032
END		247	247	248	260
STAR T AA		110	108	108	110
CHAI N ID		٧	V	∢	¥
rog ID		1shc	2nmb	2nmb	2nmb
SEQ No.		1654	1654	1654	1654

PDB annotation	REGULATION	TRANSLATION INITIATION FACTOR SUII; TRANSLATION INITIATION FACTOR	TRANSLATION INITIATION FACTOR SUII; TRANSLATION INITIATION FACTOR	HEXAMERIZATION DOMAIN	HEXAMERIZATION DOMAIN, ATPASE, TRANSPORT	CHAPERONE AAA-ATPASE, CLPY, ATP-DEPENDENT PROTEOLYSIS	PHOSPHOTRANSFERASE C-SRC, P60-SRC, RTROSINE KINASE, PHOSPHORYLATION, SH2, SH3, 2 PHOSPHOTYROSINE, PROTO-ONCOGENE,	PHOSERIO IN ANASPERANDE COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE) TRANSDUCTION/PEPTIDE), SH3	DOMAIN	
Coumpound		BIF1; CHAIN: NULL;	BIF1; CHAIN: NULL;	N-ETHYLMALEIMIDE-	SENSITIVE FUSION PROTEIN; CHAIN: A;	HEAT SHOCK PROTEIN HSLU; CHAIN: A;	TYROSINE-PROTEIN KINASE SRC; CHAIN: NULL;	GRB2; CHAIN: A; SOS-1; CHAIN: B;		PROTEIN GROWTH FACTOR RECEPTOR-BOUND PROTEIN GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (REAR, ATTEMNAL (16BR 3 SH3 DOMAIN) COMPLEXED WITH SOS-A PEPTIDE (1GBR 4 (NNR, 29 STRUCTURES) (1GBR 4 5)
SEQFOL D score		141.21								
PMF			1.00	0.36		0.13	0.45	0.17		0.59
Verify			0.42	-0.15		-0.14	-0.13	0.09		60.00
Psi Blast		1.6e-44	1.6e-44	I.6e-11		1.3e-17	4.8e-22	9.6e-15	\neg	1.6e-15
END		149	149	257		560	426	386		392
STAR T AA		29	42	186		140	334	335		38
CHAI N ID				V		A		V		⋖
PDB UI		2if)	2if)	1d2n		1g41	Ifmk	1gbq		1gbr
SEQ No B		1658	1658	1660		1660	1663	1663		1663

PDB annotation		SIGNAL TRANSDUCTION ADAPTOR SH2, SH3 1GRI 14	COMPLEX (KINASE/PEPTIDE)	TYROSINE KINASE TYROSINE KINASE-INHBITOR COMPLEX, DOWN-REGULATED KINASE, 2 ORDERED ACTIVATION LOOP	SIGNAL TRANSDUCTION PROTEIN SRC-HOMOLOGY 3 (SH3) DOMAIN, PEPTIDE-BINDING PROTEIN, 18EM 18 2 GUANING NUCLEOTIDE EXCHANGE FACTOR 18EM 19	TRANSFERASE TRANSFERASE, TYROSINB KINASE, SH3, SH2, ONCOPROTEIN	TRANSPORT PROTEIN SERING-RICH RNA POLYMERASE I SUPPRESSOR PROTEIN; ARM REPEAT	STRUCTURAL PROTEIN ARMADILLO REPEAT, BETA-
Coumpound	ADAPTOR PROTEIN CONTAINING SEZ AND SH3 CONTAINING SEZ AND SH3 GROWTH FACTOR RECEPTOR- BOUND PROTEIN Z (GREZ) IGFC 3 (C-TERMINAL SH3 DOMAIN) (NMR, MINIMIZED MEAN STRUCTURE) 16FC 4	GROWTH FACTOR BOUND PROTEIN 2; 1GRI 5 CHAIN: A, B; 1GRI 6	P56=LCK== TYROSINE KINASE; ILCK 7 CHAIN: A; ILCK 8 TAIL PHOSPHOPETIDE TEGQRPHOSPHOJYQPQP; ILCK 14 CHAIN: B; ILCK 15	HAEMATOPOETIC CELL KINASE (HCK); CHAIN: A;	SEM-5; ISEM 3 CHAIN: A, B; ISEM 5 10-RESIDUE PROLINE- RICH PEPTIDE FROM MSOS ISEM 8 CHAIN: C, D ISEM 10	ABL TYROSINE KINASE; CHAIN: NULL;	KARYOPHERIN ALPHA; CHAIN; A, B; MYC PROTO- ONCOGENE PROTEIN; CHAIN; C, D, E, F;	BETA-CATENIN; CHAIN: NULL; STRUCTURAL PROTEIN ARMADILLO REPEAT, B
SEQFOL D score								
PMF	0.83	0.35	0.28	60.0	96'0	-0.06	0.41	0.10
Verify score	0.40	-0.64	0.30	0.20	0.43	0.03	0.09	0.02
Psi Blast	6.46-15	6.4e-16	1.4e-18	1.6e-21	1.6e-16	4.8e-16	3e-05	7.5e-10
END	388	389	425	426	389	426	416	530
STAR T AA	333	304	334	333	330	327	36	107
CHAI N ID		¥	∢	٧	A		v	
FDB TD	1gfc	Igri	lick	lqef	Isem	2abl	lee4	2bct
SEQ NO:	1663	1663	1663	1663	1663	1663	1669	1669

PDB annotation	CATENIN, STRUCTURAL PROTEIN	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECONITION, BRITORE MAPPING, LEUCINE-RICH 3 REPEATS	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (THIBITOR/NUCLEASE), COMPLEX (REANG), HYDROLASE 2, MOLECULAR RECOGNITION, BETTORE MAPPING, LEUCINE-RICH 3 REPEATS	COMPLEX (NUCLEAR PROTEINRNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SYRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEINRNA) COMPLEX (NUCLEAR PROTEINRNA), RNA, SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEINRNA) COMPLEX (NUCLEAR PROTEINRNA), RNA, SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEINRNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEINRINA) COMPLEX (NUCLEAR PROTEINRINA), RNA, SNRNP, RIBONUCLEOPROTEIN
Coumpound		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, B;	RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	U2 RNA HARPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q. R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN; Q, R; U2 A'; CHAIN; A, C; U2 B"; CHAIN; B, D;	U2 RNA HAIRPIN IV; CHAIN; Q, R; U2 A'; CHAIN; A, C; U2 B"; CHAIN; B, D;
SEQFOL D score								
PMF		0.27	1.00	0.40	0.74	0.37	0.34	0.82
Verify		0.16	0.54	0.10	0.36	0.41	-0.03	0.28
Psi Blast		6.4c-12	1.5e-37	1.56-19	9.6e-07	16-23	1.5e-22	9e-20
END		362	314	301	131	171	230	301
STAR T AA		27	29	126	27	30	23	126
CHAI N ID		- A	∢	¥	4	¥	<	ပ
EDB CI		la4y	lady	la9n	la9n	la9n	la9n	1a9n
SEQ NO.		1671	1671	1671	1671	1291	1671	1691

							11	II.	13	1
PDB annotation	COMPLEX (NUCLEAR PROTEINRNA) COMPLEX (NUCLEAR PROTEINRNA), RNA, SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEIN(RNA), COMPLEX (NUCLEAR PROTEIN(RNA), RNA, SNRNP, RIBONICLEOPROTEIN	COMPLEX (NUCLEAR PROTEINRNA) COMPLEX (NUCLEAR PROTEINRNA), RNA, SNRNP, RIBONUCLEOPROTEIN	COMPLEX (NUCLEAR PROTEINRNA) COMPLEX (NUCLEAR PROTEINRNA), RNA, SNRNP, RIBONICLEOPROTEIN	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP RIBONICI EOPROTFIN	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION	TOTAL STATE OF THE PARTY OF THE
	PROTE (NUCL.	COMPI PROTE (NUCL)	COMPI PROTE (NUCL)	PROTE (NUCL)	COMPI PROTE (NUCL)	COMPL PROTE (NUCL)	CELL ADHE REPEAT, CA	CELL ADHE REPEAT, CA	CELL ADHI REPEAT, C. ADHESION	
Coumpound	UZ RNA HAIRPIN IV; CHAIN: Q, R; UZ A'; CHAIN: A, C; UZ B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN; Q, R; U2 A'; CHAIN; A, C; U2 B"; CHAIN; B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A; CHAIN: A, C; U2 B"; CHAIN: B, D;	INTERNALIN B; CHAIN: A;	INTERNALIN B; CHAIN: A;	INTERNALIN B; CHAIN: A;	The second secon
SEQFOL D score										
PMF	09:0	0:00	0.95	0.84	0.01	0.57	0.94	0.93	1.00	I
Verify	0.50	0.13	0.24	0.40	0.44	0.16	0.70	0.18	0.31	
Psi Blast	4.5e-24	0.00064	96-18	9.6e-07	9e-24	6e-23	1.6e-23	1.6e-21	6e-14	
END	299	342	334	131	174	240	290	381	901	
STAR T AA	171	216	220	27	30	23	138	173	29	000
CHAI N ID	0	o	ပ	၁	၁	υ	A	A	Ą	
PDB CI	1a9n	1a9n	1a9n	1a9n	la9n	la9n	140b	90P1	90P1	. 101
SEQ NO:	1671	1671	1671	1671	1671	1671	1671	1671	1671	

							_														
PDB annotation	REPEAT, CALCIUM BINDING, CELL ADHESION	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE,	2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT		TRANSFERASE CRYSTAL	STRUCTURE, RAB GERANYI GERANYI TRANSFERASE	2.0 A 2 RESOLUTION, N-	FORMYLMETHIONINE, ALPHA	occurri, periodocuri	TRANSFERASE CRYSTAL	STRUCTURE, RAB	20 A 2 RESOLUTION. N-	FORMYLMETHIONINE, ALPHA	SUBUNIT, BETA SUBUNIT		TRANSFERASE CRYSTAL	STRUCTURE, RAB GFRANYI GFRANYI TRANSEERASE	20 A 2 RESOLUTION N.	FORMYLMETHIONINE, ALPHA
Coumpound		INTERNALIN B; CHAIN: A;	INTERNALIN B; CHAIN: A;	RAB GERANYLGERANYLTRANSFE RASE ALPHA SUBUNIT;	CHAIN: A, C, RAB GERANYLGERANYLTRANSFE RASE BETA SUBUNIT; CHAIN:	B, D;	RAB	GERANYLGERANYLTRANSFE RASE ALPHA SHRIMIT:	CHAIN: A, C; RAB	GERANYLGERANYLTRANSFE RASE BETA SUBINIT: CHAIN:	B, D;	RAB	GEKANYLGEKANYLIKANSFE DASE ALBUA STIDLINET:	CHAIN: A. C. RAB	GERANYLGERANYLTRANSFE	RASE BETA SUBUNIT; CHAIN:	B, D;	RAB	GERANYLGERANYLTRANSFE RASE AI PHA SUBLINIT.	CHAIN: A C. RAB	GERANYLGERANYLTRANSFE
SEQFOL D score																					
PMF score		00'1	0.1	1.00			0.36					1.00						0.89			
Verify		0.74	19:0	0.49			0.18					99.0						9.08			
Psi Blast		1.3e-27	8e-28	4.8e-14			3.2e-06					4.8e-10						4.8e-12			
END AA		961	242	250			107					130						154			
STAR T AA		43	70	145			_					27						84			
CHAI N ID		A	V	¥			٧					Ą						ν.			
PDB CD		140b	90P1	1 dce			1dce					Idce						ldce			
SEQ No ID		1671	1671	1671			1671					1/91						1671			

PDB annotation	SUBUNIT, BETA SUBUNIT	CONTRACTILE PROTEIN LEUCINE- RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHIAMYDOMONAS, FLAGELLA	CONTRACTILE PROTEIN LEUCINE- RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA	CONTRACTILE PROTEIN LEUCINE- RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA	CONTRACTILE PROTEIN LEUCINB- RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA	CONTRACTILE PROTEIN LEUCINE- RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA	SIGNALING PROTEIN PHOTORECREPTOR, G PROTEIN- COUPLED RECEPTOR, MEMBRANE PROTEIN, 2 RETINAL PROTEIN, VISUAL PROMENT	RNA BINDING PROTEIN TAP (AFXI); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH- REPEAT 2 (LRR)	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-
Coumpound	RASE BETA SUBUNIT; CHAIN: B, D;	OUTER ARM DYNEIN; CHAIN: A;	OUTER ARM DYNEIN; CHAIN: A;	OUTER ARM DYNEN; CHAIN: A;	OUTER ARM DYNEIN; CHAIN: A;	OUTER ARM DYNEIN; CHAIN: A;	RHODOPSIN; CHAIN: A, B	NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;
SEQFOL D score									
PMF		0.11	69.0	10:0	0.64	0.52	0.05	0.72	0.22
Verify		-0.03	-0.14	-0.32	0.03	0.09	-0.04	0.27	-0.08
Psi Blast		1.6e-13	1.4e-21	6.4e-10	1.6e-12	3.2e-16	1.5e-14	8e-05	1.1e-05
END		289	299	380	148	561	702	83	107
STAR T AA		154	165	201	27	59	403	27	45
CHAI N ID		¥	¥	٧	₹	V	g	٧	٧
PDB		1ds9	lds9	1ds9	1ds9	1ds9	1188	lfol	1fo1
SEQ NO.		1671	1671	1671	1671	1671	1671	1671	1671

PDB annotation	REPEAT 2 (LRR) RNA BINDING PROTEIN TAP (NFX1);	KIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH- REPEAT 2 (LRR)	TRANSCRIPTION RNA IP; RANGAP; GTPASE-ACTIVATING PROTEIN	FOR SPII, GTPASE-ACTIVATING	LRR, LEUCINE-2 RICH REPEAT	PROTEIN, TWINNING,	MEROHEDRAL I WINNING, 3	MEROHEDRY	ACETYLATION RNASE INHIBITOR,	PHILIDINGS A CERTAIN ATION	LEUCINE-RICH REPEATS	ACETYLATION RNASE INHIBITOR,	RIBONUCLEASE/ANGIOGENIN	INHIBITOR ACETYLATION,	LEUCINE-RICH REPEATS	ACETYLATION RNASE INHIBITOR,	INHIBITOD ACETYL ATION	LEUCINE-RICH REPEATS	LIGASE SKP2 F-BOX; SKP1; SKP1,	SKP2, F-BOX, LRR, LEUCINE-RICH	REPEAT, SCF, UBIQUITIN, 2 E3,	UBIQUITIN PROTEIN LIGASE	LIGASE SKP2 F-BOX; SKP1; SKP1,	SKP2, F-BOX, LRR, LEUCINE-RICH	REPEAT, SCF, UBIQUITIN, 2 E3,
Coumpound	NUCLEAR RNA EXPORT	FACTOR I; CHAIN: A, B;	GTPASE-ACTIVATING PROTEIN RNA1_SCHPO;	CHAIN: A, B;					RIBONUCLEASE INHIBITOR;	CHAIN TOUCH		RIBONUCLEASE INHIBITOR;	CHAIN: NULL;			RIBONUCLEASE INHIBITOR;	CITATIN INOTES,		CYCLIN A/CDK2-ASSOCIATED	P19; CHAIN: A, C; CYCLIN	A/CDK2-ASSOCIATED P45;	CHAIN: B, D;	CYCLIN A/CDK2-ASSOCIATED	P19; CHAIN: A, C; CYCLIN	A/CDK2-ASSOCIATED P45;
SEQFOL D score																									
PMF	06'0		0.25						89.0			0.21				00:			0.34				0.59		7
Verify	0.32		-0.01						0.41			0.19				0.33			-0.85				-0.62]
Psi Blast	1.1e-05		1.5e-16						6e-50			1.4e-16				3e-31			1.6e-08				1.3e-08		
END	107		154						314			424				334			139				62		
STAR T AA	45		82						53			30			00	3			8		_		35		
CHAI N ID	м		∢																٧				٧		
EDB ID	[fo]		lyrg						2buh			2bnh				uuq7			ItsI				Its		1
SEQ No. 10	1671		1671						1671			1671			1000	16/1			1673				1673		1

PDB annotation	UBIQUITIN PROTEIN LIGASE	LIGASE CYCLIN ACDIX-A ASSOCIATED P45, CYCLIN ACDIX- ASSOCIATED P19, SKP1, SKP2, F- BOX, LRSS, LEUCINE-ROCH REPEATS, SCF2, USIQUITIN, E3, BOQUITIN PROTEIN LIGASE	TRANSFERASE ALLOSTERY, COOPERATIVITY, GLYCEROL KINASE, CRYSTAL 2 STRUCTURE, TRANSFERASE	TRANSFERASE ALLOSTERY, COOPERATIVITY, GLYCEROL	KINASE, CRYSTAL 2 STRUCTURE, TRANSFERASE	ANTIFUNGAL PROTEIN OSMOTIN- LIKE PROTEIN; ANTIFUNGAL PROTEIN, PATHOGENESIS-	RELATED PROTEIN, PR-5D, 2 OSMOTIN, THAUMATIN-LIKE PROTEIN	HYDROLASE INHIBITOR ALL-BETA STRUCTURE, HYDROLASE INHIBITOR	HYDROLASE INHIBITOR ALL-BETA STRUCTURE, HYDROLASE INHIBITOR	HYDROLASE INHIBITOR ALL-BETA STRUCTURE, HYDROLASE INHIBITOR	HYDROLASE INFIBITOR ALL-BETA STRUCTURE, HYDROLASE
Coumpound	CHAIN: B, D;	SKP2, CHAIN: A, C; SKP1; CHAIN: B, D;	GLYCEROL KINASE; CHAIN: O, Y, Z, X;	GLYCEROL KINASE; CHAIN: 0, Y, Z, X;		PR-5D; CHAIN: NULL;		BOWMAN-BIRK TRYPSIN INHIBITOR; CHAIN: A	BOWMAN-BIRK TRYPSIN INHIBITOR; CHAIN: A	BOWMAN-BIRK TRYPSIN INHIBITOR; CHAIN: A	BOWMAN-BIRK TRYPSIN INHIBITOR; CHAIN: A
SEQFOL D score				310.87		52.19					
PMF		. 0.28	1.00					60:0	0.00	-0.14	-0.18
Verify score		-0.51	0.56					-0.16	1.29	1.60	0.79
Psi Blast		6.4e-09	0	0		0.009		4.5e-17	60-16	6e-15	3e-I9
END		162	491	492		161		201	162	118	197
STAR		06	18	81		_		134	42	4	84
CHAI		<	0	0				<	<	<	V
EDB CI		162	1bu6	9nqI		laun		1c2a	1c2a	1c2a	1c2a
SEQ No.		1673	1675	1675		9291		1676	1676	1676	1676

S e S	ED CI	CHAI	STAR	END	Psi Blast	Verify score	PMF	SEQFOL D score	Coumpound	PDB annotation
										INHIBITOR
1676	1ehd	₹	104	192	1,2e-17	0.87	0.01		AGGLUTININ ISOLECTIN VI; CHAIN: A	PLANT PROTEIN TWO HOMOLOGOUS HEVEIN-LIKE DOMAINS
1676	1ehd	<	10	100	1.2e-19	1.43	-0.14		AGGLUTININ ISOLECTIN VI; CHAIN: A	PLANT PROTEIN TWO HOMOLOGOUS HEVEIN-LIKE DOMAINS
1676	lehd	4	84	172	3e-18	1.28	-0.12		AGGLUTININ ISOLECTIN VI; CHAIN: A	PLANT PROTEIN TWO HOMOLOGOUS HEVEIN-LIKE DOMAINS
1676	leis	¥	01	116	1.5e-18	1.17	-0.18		AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V; CHAIN: A;	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN
1676	Ieis	٧	124	192	1.3e-14	0.05	-0.12		AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V; CHAIN: A;	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN
1676	1eis	V	ço.	98	7.5e-18	1.32	0.15		AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V; CHAIN: A;	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN
1676	leis	V	29	142	1.5e-19	1.70	-0.14		AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V; CHAIN: A;	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN
1676	leis	¥	11	172	3e-18	1.37	-0.17		AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V; CHAIN: A;	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN
1676	len2	A	104	192	le-18	86.0	-0.14		AGGLUTININ ISOLECTIN I/AGGLUTININ ISOLECTIN V/ CHAIN: A;	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN, SACCHARIDE BINDING
1676	len2	V	10	901	3e-17	1.34	-0.12		AGGLUTININ ISOLECTIN 1/AGGLUTININ ISOLECTIN V/ CHAIN: A;	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN, SACCHARIDE BINDING
1676	len2	Ą	3	98	1.1e-16	1.29	0.15		AGGLUTININ ISOLECTIN	SUGAR BINDING PROTEIN UDA;

	_			_	_	$\overline{}$		_			
PDB annotation	LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN, SACCHARIDE BINDING	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN, SACCHARIDE BINDING	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN	HORMONE RECEPTOR HORMONE RECEPTOR, INSULIN RECEPTOR FAMILY	GLYCOPROTEIN GLYCOPROTEIN	GLYCOPROTEIN GLYCOPROTEIN	GLYCOPROTEIN GLYCOPROTEIN	SIGNALLING PROTEIN TYPE I RECEPTOR, STNFR1; INCF 8 BINDING PROTEIN, CYTOKINE INCF 19	OUTER MEMBRANE PROTEIN OSMOPORIN; OUTER MEMBRANE PROTEIN, NON-SPECIFIC PORIN, OSMOPORIN, 2 BETA-BARREL, TRANSMEMBRANE	COMPLEX (BLOOD COAGULATION/NIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIAAEGF, BLOOD COGGILL/TON, 2 PLASMA, SERINE ROTTASE. CALCIIM.
Coumpound	VAGGLUTININ ISOLECTIN V/ CHAIN: A;	AGGLUTININ ISOLECTIN VAGGLUTININ ISOLECTIN V/ CHAIN: A;	TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	INSULIN-LIKE GROWTH FACTOR RECEPTOR 1; CHAIN: A:	LAMININ; CHAIN: NULL;	LAMININ; CHAIN: NULL;	LAMININ; CHAIN; NULL;	TUMOR NECROSIS FACTOR RECEPTOR; INCF 4 CHAIN: A, B; INCF 5	OMPK36; CHAIN: A, B, C;	FACTOR IXA; CHAIN: C, L.; D- PHB-PRO-ARG; CHAIN: 1;
SEQFOL D score			59.75					84.67	50.00		
PMF		0.01		-0.19	-0.20	50'0	-0.15			-0.20	-0.20
Verify score		1.54		0.74	0.85	1.09	1.39			1.57	0.33
Psi Blast		3e-18	3e-15	3e-15	6e-25	3e-25	6e-24	3e-25	11-91	4.5e-14	4.5e-19
END		172	661	197	200	199	159	160	200	138	201
STAR T AA		74	47	49	10	35	3	4	46	20	42
CHAI		V	4	4	Ą				∢	∢	T
PDB		len2	lext	lext	Tigi.	Iklo	ıklo	Iklo	lncf	losm	lpfx
SEQ B S		9/91	9291	9291	1676	1676	1676	1676	1676	1676	9.291

PDB annotation	BINDING, HYDROLASE, 3 GLYCOPROTEIN	MEMBRANE ADHESION SHORT CONSENSUS REPEAT, SUSHI,	COMPLEMENT CONTROL PROTEIN,	2 N-GLYCOSYLATION, MULTI-	SERINE PROTEASE INHIBITION	FACTOR XA INHIBITOR;	ANTISTASIN, CRYSTAL	STRUCTURE, FACTOR XA	INHIBITOR, 2 SERINE PROTEASE NHIBITOR THE OMBOSIS	SERINE PROTEASE INHIBITOR	FACTOR XA INHIBITOR:	ANTISTASIN, CRYSTAL	STRUCTURE, FACTOR XA	INHIBITOR, 2 SERINE PROTEASE	NHIBITOR, THROMBOSIS	SERINE PROTEASE INHIBITOR	FACTOR XA INHIBITOR;	ANTISTASIN, CRYSTAL	STRUCTURE, FACTOR XA	INHIBITOR, 2 SERINE PROTEASE	NHIBITOR, THROMBOSIS	SERINE PROTEASE INHIBITOR	FACTOR XA INHIBITOR;	ANTISTASIN, CRYSTAL	STRUCTURE, FACTOR XA	NHIBITOR, 2 SERINE PROTEASE	NHIBITOR, THROMBOSIS		
	BINI	MEN	COM	Z 2	SER	FAC	AN	STR		SER	FAC	ANT	STR	E	E	SERI	FAC	ANT	STR	E	EN	SERI	FAC	ANT	STR	E	H		
Coumpound		HUMAN BETA2- GLYCOPROTEIN I: CHAIN: A:			ANTISTASIN; CHAIN: NULL;					ANTISTASIN: CHAIN: NULT:	Ì					ANTISTASIN; CHAIN: NULL;						ANTISTASIN; CHAIN: NULL;						MEMBRANE PROTEIN	OUTER LAYER PROTEIN I
SEQFOL D score																						66.09							
PMF		-0.20			-0.15					0.29						-0.12												-0.20	
Verify score		0.83			0.92					1.27						0.53												1.30	
Psi Blast		1.4e-30			6e-15					1.1e-15						6e-21						6e-21						1.5e-14	
END		200			168					175						198						202						107	
STAR T AA		6			13					74				_		83						83							
CHAI N ID		V																										×	
PDB		Iqub			Iskz					Iskz						lskz						Iskz						lvmo	
SEQ 10 NO:		1676			1676					1676						1676						1676						1676	

								_					_									
			OXIDOREDUCTASE ALPHA-BETA- ALPHA MOTIF, FLAVIN CONTAINING PROTEIN, OXIDASE	FLAVOENZYME FLAVOENZYME, NAD BIOSYNTHESIS, FAD, OXIDOREDUCTASE	OXIDOREDUCTASE ADR, NADPH:	OXIDOREDUCTASE:	FLAVOENZYME, MAD ANALYSIS, ELECTRON TRANSFERASE	OXIDOREDUCTASE TETRAHEME	FLAVOCYTOCHROME C	FUMARATE REDUCTASE, 2 OXIDOREDICTASE	OXIDOREDUCTASE IRON-SULFUR	FLAVOPROTEIN, ELECTRON	IRANSFER, UXIDOREDUCTASE	OXIDOREDUCTASE IRON-SULFUR	TRANSFER, OXIDOREDUCTASE	OXIDOREDUCTASE LIPOAMIDE	DEHYDROGENASE, L PROTEIN, E3,	DEDA, DIRTDROLLPOAMIDE	COLUMN O DE COMPANIO DE LA COLUMN DE LA COLUMN DE LA COLUMN DE COLUMN DE LA COLUMN	DEHYDROGENASE COMPLEX	GLYCINE 3 DECARBOXYLASE	COMPLEX, FLAVOPROTEIN
1VMO 3	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3		D-AMINO ACID OXIDASE; CHAIN: A;	L-ASPARTATE OXIDASE; CHAIN: A;	ADRENODOXIN REDUCTASE;	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		FLAVOCYTOCHROME C	FUMARATE REDUCTASE;	CHAIN: A;	TRIMETHYLAMINE	DEHYDROGENASE; CHAIN: A,		TRIMETHYLAMINE DEHYDPOGENASE: CHAIN: A	B;	DIHYDROLIPOAMIDE	DEHYDROGENASE; CHAIN: A,	3, C, D;				
	101.83				62.05																	
			0.19	0.13				0.36			0.12			0.70		0.00						
			-0.46	-0.05				-0.03			-0.09			-0.08		-0.41						
	4.5e-23		0.00048	0.00014	3.2e-37			3.2e-09			1.6e-12			9e-13		0.003						
	681		39	46	457			318			182		4	329		118						
	8		=	7	10			142			2			ς.		2			_	_		
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	9мва		1с0р	lchu	leje			1d4d			Idin			Idju		ldxl						
	9291		1680	1680	1680			1680			1680		0000	1680		1680						
		9wga A 8 189 4.5e-23 101.83	9vgs A 8 189 4.5-2.23 101.83	Jorga A 8 189 4.5c.23 101.83 IVMO3 IVMO3 ARACALJTININ WHEAT REM AGGALJTININ GREM AGGALJTININ (ISCLECTINI) GREM AGGALJTININ (ISCLECTINI) JORGANIA J	1996 A 8 189 4.5e.23 101.83 1.WAO3 1.WAO3 1.WAO3 1.ECTIN AGGLJJTINUN WHEAT 1040	1996 A 8 189 4.5e.23 101.83 119M.03 119M.03 119M.03 119M.04 A A A A A A A A A	Joyga A 8 189 4.5e-23 101.83 IVMO3 APPLATIONIN WHEAT 1cop A 11 39 0.00048 -0.46 6.19 D-AMINO ACID OXIDASE; 1cbu A 7 46 0.00014 -0.05 0.13 L-ASPARTATE OXIDASE; 1cjc A 10 457 3.2e-37 62.05 ADBENOXIN REDUCTASE; 1cjc A 10 457 3.2e-37 62.05 CHAIN; A;	10 10 10 10 10 10 10 10	10 10 10 10 10 10 10 10	190ga	10 14 142 118 136-14-13 101.83 11.00.0 1	10 10 10 10 10 10 10 10	100 20 110 20 100 20 100 20 100 20 100 20 2	10.183 189 4.5e.23 10.183 11.WO3 10.WO3 10.183 11.WO3 10.183 11.WO3 10.183 11.WO3 10.183 10.	10 10 10 10 10 10 10 10	10 10 10 10 10 10 10 10	10.183 11.00.03	100 8 189 4.5e.23 101.83 11VVO3 100.0000 100.000 100.000 100.0000 100.0000 100.0000 100.0000 100.0000 100.	10 8 189 4.5e.23 101.83 10.WO3 10.	10 10 10 10 10 10 10 10	101.83 17W/03 1	101.83 11WO3 11W

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PDB annotation	FLAVOPROTEIN, FAD, NADP	FLAVIN FLAVIN, PHENOL HYDROXYLASE, MONOOXYGENASE, OXIDOREDUCTASE	COMORED UCTORS COMPLEX I; COMPLEX II; COMPLEX II; COMPLEX II; FINARAT II; SUCCINATE DEPTO COMPLEX II; SUCCINATE DEPTO COMPLEX II SUCCINATE DEPTO COMPLEX II.	TOWNER OWEUEX II; COMPILEX II; COMPILEX II; EVANCHEX II; REDUCTASE, COMPILEX II SUCCINATE DEHYDROGENASE, 2 RESPIRATION, OXIDOREDUCTASE		
Coumpound		PHENOL HYDROXYLASE; CHAIN: A, B, C, D;	THOMAN, TREDUCTARE FLAVOPROTEIN SIBENUT: CAUNEA, AN, FTHANRACHE REDUCTARE INON-SULFUR PROTEIN'S CHARIE, BI, FROMENTE REBUCTARE IS AD HYDROPHOBIC PROTEIN'S FROMENTE REPUCTARE IS AD HYDROPHOBIC PROTEIN'S REDUCTARE IS AD HYDROPHOBIC PROTEIN'S FROMENTE IS AD HYDROPHOBIC PRO	THOMANCE REDUCTASE THANOPROTEIN SUBUNIT: CEMBER, AN FURMARATE REDUCTASE REMOCRATIFUR PROTEIN; CHAIN; B, N; PROTEIN; CHAIN; B, N; PROTEIN; CHAIN; B, N; PROTEIN; CHAIN; C, EUMAKATE REDUCTASE 13 KD	OXIDOREDUCTASE DIHYDROLIPOAMIDE DEHYDROGENASE (E.1.8.1.4) COMPLEX WITH IL.PF 3. FLAVIN-ADENINE DINUCLEOTIDE (FAD) IL.PF 4.	OXIDOREDUCTASE
SEQFOL D score						
PMF		0.05	0.37		0.15	0.04
Verify score		-0.79	-0.74	-0.56	-0.25	-0.14
Psi Blast		0.00032	3.2e-06	0.00032	3.2e-95	3.2e-75
END		43	43	391	462	462
STAR T AA		12	12	310	80	13
CHAI		¥	∢	4	¥	
FDB ID		qoji	Ifum	Ifum	Ilpf	IIVI
SEQ No: D		1680	1680	1680	1680	1680

PDB annotation		-	OXIDOREDUCTASE REDOX-ACTIVE CENTER, GLYCOLYSIS, OXIDOREDUCTASE, NAD, 2 FLAVOPROTEIN, FAD, P64K	OXIDOREDUCTASE OXIDOREDUCTASE, OXIDOREDUCTASE, NAD	OXIDOREDUCTASE OXIDOREDUCTASE		TRANSCRIPTION INHIBITOR BETA- PROPELLER	TRANSCRIPTION INHIBITOR BETA- PROPELLER	COMPLEX (GTP- BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT;
Coumpound	DIHYDROLIPOAMIDE DEHYDROCENASE (E.C.1.8.1.4) COMPLEX WITH 1LVL 3 NICOTINAMIDE-ADENINE- DINUCLEOTIDE (NAD+) 1LVL 4	OXIDOREDUCTASE (H2O2(A)) NADH PEROXIDASE (HPX) (E.C.I.I.I.) MUTANT WITH CYS 42 INHP 3 REPLACED BY ALA (CAZA) INHP 4	SURFACE PROTEIN; CHAIN: NULL;	L-ALANINE DEHYDROGENASE; CHAIN: A;	FLAVOCYTOCHROME C3 FUMARATE REDUCTASE; CHAIN: A, D;	OXIDOREDÚCTASE DIHYDROLIPOAMIDE DEHYDROGENASE (E.C.1.8.1.4) 31.AD 3	TRANSCRIPTIONAL REPRESSOR TUPI; CHAIN: A, B, C;	TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	GT-ALPHA/GI-ALPHA CHIMERA; CHAIN: A; GT- BETA; CHAIN: B; GT-GAMMA;
SEQFOL D score		76.88							
PMF			0.22	0.11	90:0	0.35	10.0	0.99	-0.14
Verify			90'0-	0.02	-0.43	-0.06	0.25	0.56	0.43
Psi Blast		1,6e-57	6.4e-88	0.0048	6.4e-05	3.2c-91	1.6e-61	3.2e-72	1.4e-55
END		418	463	177	49	462	479	624	476
STAR T AA		21	9	145	4	∞	173	304	155
CHAI N ID				¥	A	4	A	<	В
PDB ID		dyu[10jt	1pjc	1408	3lad	lerj	lerj	lgot
SEQ No. 10		1680	1680	0891	1680	1680	1681	1881	1891

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PDB annotation	GAMMAI, TRANSDUCIN GAMMA SUBUNIT, COMPLEX (GTP- BINDINGTRANSDUCER), G PROTEIN, HETEROTRIMER 2 SIGNAL TRANSDUCTION	COMPLEX (GTP- BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBINIT; GAMAA, TRANSDUCIN GAMAA SUBUNIT; COMPLEX (GTP- BINDING/TRANSDUCER), PROTRIA, IBETROTRIMER Z SIGNAL TRANSDUCTION	COMPLEX (GTP. BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNIT; GAMMAI, TRANSDUCIN GAMMA SUBUNIT; CONPLEX (GTP. BINDING/TRANSDUCER), G PROFIN, HETEROTRIMER 2 SIGNAL, TRANSDUCTION		OUTER MEMBRANE PROTEIN OSMOPORIN; OUTER MEMBRANE PROTEIN, NON-SPECIFIC PORIN, OSMOPORIN, 2 BETA-BARREI, TRANSMEMBRANE	OUTER MEMBRANE PROTEIN OSMOPORIN, OUTER MEMBRANE PROTEIN, NON-SPECIFIC PORIN, OSMOPORIN, 2 BETA-BARREL, TRANSMEMRANE	
Coumpound	CHAIN; G;	GT-APPAGG-ALPHA CHIMERA; CHAIN: A; GT- BET4; CHAIN: B; GT-GAMMA; CHAIN: G;	GT-ALPHAGG-ALPHA CHIMERA; CHAIN: A; GT- BETA; CHAIN: B; GT-GAMMA; CHAIN: G;		OMPK36; CHAIN: A, B, C;	OMPK36; CHAIN: A, B, C;	OUTER MEMBRANE PROTEIN PHOSPHOPORIN (PHOE) 1PHO 3
SEQFOL D score		74.60					
PMF			0.71		-0.20	-0.18	-0.20
Verify			0.76		0.86	Ξ	0.90
Psi Blast		1.46-55	3.2e-74		4.5e-10	1.56-12	1.2e-11
END AA		524	621		67	18	08
STAR T AA		179	302		vo.	∞	4
CHAI N ID		м	ш		∢	¥	
PDB ID		1got	lgot		nson	losm	Ipho
SEQ NO:		1681.	1681		1685	1685	1685

CHAI N ID		STA T A	e <	8 4	Psi Blast	Verify	PMF	SEQFOL D score	Coumpound	PDB annotation
2omf 8 80 1.3e-10	80	80		1.3e-10	_	1.14	-0.19		MATRIX PORIN OUTER MEMBRANE PROTEIN F; 20MF 5 CHAIN: NULL; 20MF 6	INTEGRAL MEMBRANE PROTEIN PORIN MATRIX PORIN, OMPF PORIN; 20MF 7 PORIN, MEMBRANE PROTEIN 20MF 12
1cun A 98 210 0.00015	98 210	210	1	0.00013	1	-0.05	0.04		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2.2 ANDERS ATTER TO COLUMN
										STRUCTURAL PROTEIN
Jut 14 124 9.6e-27	124	124		9.6e-27		-0.02	0.22		HYDROLASE CYTIDINE DEAMINASE (CDA) (E.C.3.5.4.5) COMPLEXED WITH ICTT 3.3,4- DIHYDROZEBULARINE (DHZ) ICTT 4	
la6d A 15 186 80-55	15 186	981		8e-55		-0.12	1.00		THERMOSOME; CHAIN: A, B;	CHAPERONIN THERMOPLASMA ACIDOPHILUM, GROUP II CHAPERONIN, CCT, TRIC, 2 PROTEIN FOI DING ATPASE
la6d B 20 186 6.4e-51	20 186	186		6.4e-51		-0.29	1.00		THERMOSOME; CHAIN: A, B;	CHAPERONIN THERMOPLASMA ACIDOPHILUM, GROUP II CHAPERONIN, CCT. TRIC, 2
										PROTEIN FOLDING, ATPASE
1der A 12 186 1.6e-68	12 186	186		1.6e-68		-0.14	0.72		GROEL; CHAIN: A, B, C, D, B, F, G, H, I, J, K, L, M, N;	CHAPERONIN HSP60 CLASS, ATP, MAGNESIUM, CHAPERONIN
1pkl A 5 106 0.0008	5 106	901		0.0008		-0.18	0.23		PYRUVĀTE KINĀSE; CHAIN: A, B, C, D, E, F, H, Q;	TRANSFERASE PYRUVATE KINASE, GLYCOLYTIC ENZYME, HOMOTETRAMER, 2 TRANSFERASE
laih A 33 114 1.4e-09	33 114	114		1.4e-09		0.06	-0.19		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OI IGONICI ROTIDE BINDING	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER DNA-BINDING
					7				CONTROL OF THE CONTRO	CHACLE PROPERTY OF THE PARTY OF

PDB annotation	PROTEIN	COMPLEX (ZINC FINGER/DNA),	ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	IN LEKACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	_	-	REGULATION/DNA) TFIIIA; 5S	GENE; NMR, TFIIIA, PROTEIN, DNA,	TRANSCRIPTION FACTOR, 5S RNA 2	GENE, DNA BINDING PROTEIN,	ZINC FINGER, COMPLEX 3	(TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-YANG 1;	TRANSCRIPTION INITIATION,	INITIATOR ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-PROTEIN
Coumpound	SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX	OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;		DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			TRANSCRIPTION FACTOR IIIA;	CHAIN: A; 5S RNA GENE;	CHAIN; E, F;						YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;	
SEQFOL D score																									i					
PMF		-0.14		-0.18				-0.17					-0.12					-0.19								-0.14				
Verify		0.07		20.0				0.10					0.16					80.0								0.04				
Psi Blast		6.4e-27		3.2e-19				8e-35					1.Ie-09					1.4e-13								3.2e-28				
END AA		168		114				142					114					138								168				
STAR T AA		8		31				19					87					69								63				
CHAI N ID		∢		Ü				၁					Ö					٧								U				
EDB CI		lalh		lmey				1mcy					lmey					2								Inbd				
SEQ NO:		1696		1696				1696					9691					1696								1696				

田田	CHAI	STAR T AA	END	Psi Blast	Verify score	PMF	SEQFOL D score	Coumpound	PDB annotation
	_								(TRANSCRIPTION REGULATION/DNA)
٧		7	144	4.8e-17	0.03	-0.11		ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)
∢		18	115	6.4e-13	0.03	0.94		U2 RNA HAIRPIN IV; CHAIN: Q. R; U2 A; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEINRNA) COMPLEX (NUCLEAR PROTEINRNA), RNA, SNRNP, RIBONUCLEOPROTEIN
Ą		43	140	6e-11	-0.34	0.00		U2 RNA HAIRPIN IV; CHAIN; Q. R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B. D.	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX ANTICLEAR PROTEIN/RNAY PNA
	_							1	SNRNP, RIBONUCLEOPROTEIN
o		8	115	6.4e-13.	0.29	96'0		U2 RNA HAIRPIN IV; CHAIN: Q.	COMPLEX (NUCLEAR
								R; U2 A; CHAIN: A, C; U2 B"; CHAIN: B, D;	PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP.RIBONUCLEOPROTEIN
٧		18	140	1.4e-28	0.51	1.00		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
4	Ī	14	114	3.2e-15	89.0	1.00		RAB	TRANSFERASE CRYSTAL
			_					GERANYLGERANYLTRANSFE	STRUCTURE, RAB
								KASE ALPHA SUBUNIT; CHAIN: A. C. RAB	GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION. N-
								GERANYLGERANYLTRANSFE	FORMYLMETHIONINE, ALPHA
								RASE BELA SUBUNIT; CHAIN: B, D;	SUBUNIT, BETA SUBUNIT
٧		39	137	3.2e-17	0.22	1:00		RAB	TRANSFERASE CRYSTAL
								GERANYLGERANYLTRANSFE RASE ALPHA SUBTINIT:	STRUCTURE, RAB GERANYI GERANYI TRANSFERASE
								CHAIN: A, C; RAB	2.0 A 2 RESOLUTION, N-
	٦							GERANYLGERANYLTRANSFE	FORMYLMETHIONINE, ALPHA

		편 참	ė .	Ä,			4 4	4 4	
PDB annotation	SUBUNIT, BETA SUBUNIT	CONTRACTILE PROTEIN LEUCINE- RICH REPEAT, BETA-BETA-ALPHA CYLNDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA	THE ANSCRIPTION REAL IP, RANGAP, THE ASSOCIATION REAL ACTIVATING PROTEIN, CAPA SHALL FANDAR REAL REAL REAL REAL REPEAT REAL RECHENTANTING, STREET WITHER REAL TWINNING, STREET REAL TRINNING, STREET REAL TWINNING, STREET STREET REAL TWINNING, STREET	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS	ENDOCYTOSIS/EXOCYTOSIS SUPERHELIX OF HELICES	ENDOCYTOSIS/EXOCYTOSIS SUPERHELIX OF HELICES	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPIEX	GENE PEGILI ATTONIONA BOLVAN
Coumpound	RASE BETA SUBUNIT; CHAIN: S B, D;	OUTER ARM DYNEIN; CHAIN: R A;	CHAIN A, B, CHAIN A, CHAIN	RIBONUCLEASE INHIBITOR; A CHAIN: NULL; R R II I	TARGET OF MYB1; CHAIN: A, E	TARGET OF MYBI; CHAIN: A, B;	SXI-LETHAL PROTEIN, CHAIN: R A, B; RNA (5:- R(P*GP*UP*UP*UP*UP*) R UP*UP*UP*UP*UP. CHAIN: P, Q;		+-
SEQFOL D score									
PMF		0.24	0.21	0.49	1.00	1.00	-0.06	1.00	51.6
Verify		-0.55	-0.36	0.06	0.84	0.78	60:0	96'0	0.05
Psi Blast		8e-23	36-09	9.6e-10	1.4e-44	1.2e-56	1.46-22	6.4e-30	3.2e-31
END		142	133	139	141	143	268	481	307
STAR		25		1	2	2	126	328	128
CHAI N ID		∢	∀		V	A	A	¥	¥
PDB ID		6sp1	lyrg	2bnh	leik	lelk	1b7f	167£	-
SEQ ID NO:		1698	1698	1698	6691	6691	1700	1700	1700 lcvj

PDB annotation	BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	GENE REGULATIONRIN, POLY(A) BINDING PROTEIN I, PABP 1; RRM, PROTEIN-RIVA COMPLEX, GENE REGULATIONRINA	GENB REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN/RNA COMPLEX, GENE REGULATION/RNA	GENE REGULATIONRNA POLY(A) BINDING PROTEIN 1, PABP 1, SRM, PROTEIN-THA COMPLEX, GENE REGULATIONRNA	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
Соимроиид	PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'*) R(*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*A); CHAIN: M, N, O, P, Q, R, S, T,	POL YDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*3); CHAIN: M, N, O. P, Q, R, S, T;	POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*A	POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA G's. R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP* AP*AP*AP*AP*AP* AP*AP*AP*AP* AP*AP*AP*AP*AP* AP*AP*AP*AP* AP*AP*AP*AP*AP* AP*AP*AP*AP*AP* AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*A	POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H, RNA (5'- R(*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP; CHAIN: M, N, AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*A	POLYDENYLATE BINDING PROTEIN I; GHANI: A, B, C; D, E, F, G, H; RNA (5- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*A
SEQFOL D score						
PMF		0.93	00.1			00.1
Verify		69'0	1.28	0.99	0.98	1.29
Psi Blast		4.8e-19	4.5e-28	4.8e-25	4.5e-24	4.8e-24
END AA		411	485	487	468	473
STAR T AA		310	331	331	331	331
CHAI		¥	∢	¥	B	В
PDB 10		levj	1cvj	levj	levj	lcvj
SEQ No. 15		1700	1700	1700	1700	1700

	_			_	_	_	_					_	_					_			_			_	_	_	_		_	
PDB annotation		GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM.	PROTEIN-RNA COMPLEX, GENE	REGULATION/RNA			GENE REGULATION/RNA POLY(A)	BINDING PROTEIN 1, PABP 1; RRM,	PROTEIN-RNA COMPLEX, GENE	REGULATION/RNA			GENE REGULATION/RNA POLY(A)	BINDING PROTEIN 1, PABP 1; RRM,	PROTEIN-RNA COMPLEX, GENE	REGULATION/RNA			RNA BINDING PROTEIN RNA- BINDING DOMAIN	RNA BINDING PROTEIN RNA- BINDING DOMAIN	RNA BINDING PROTEIN RNA-	BINDING DOMAIN	RIBONUCLEOPROTEIN UIA117;	RIBONUCLEOPROTEIN, RNP	DOMAIN, SPLICEOSOME	STRUCTURAL PROTEIN PROTEIN	C23; RNP, RBD, RRM, RNA BINDING	DOMAIN, NUCLEOLUS	NUCLEAR PROTEIN	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1.
Coumpound	O, P, Q, R, S, T;	POLYDENYLATE BINDING PROTEIN I: CHAIN: A. B. C. D.	E, F, G, H; RNA (5'-	R(*AP*AP*AP*AP*AP*AP*AP*	AP*AP*AP*A)-3'); CHAIN: M, N,	O, P, Q, R, S, T;	POLYDENYLATE BINDING	PROTEIN I; CHAIN: A, B, C, D,	E, F, G, H; RNA (5'-	R(*AP*AP*AP*AP*AP*AP*	AP*AP*AP*A)-3'); CHAIN: M, N,	O, P, Q, R, S, T;	POLYDENYLATE BINDING	PROTEIN 1; CHAIN: A, B, C, D,	E, F, G, H; RNA (5'-	R(*AP*AP*AP*AP*AP*AP*	AP*AP*AP*A)-3'); CHAIN: M, N,	O, P, Q, R, S, T;	HU ANTIGEN C; CHAIN: A;	HU ANTIGEN C; CHAIN: A;	HU ANTIGEN C; CHAIN: A;		UI SMALL NUCLEAR	RIBONUCLEOPROTEIN A;	CHAIN: NULL;	NUCLEOLIN RBD2; CHAIN: A;			HNRNP AI; CHAIN: NULL;	
SEQFOL D score																														
PMF		0.64					0.07						9.						0.71	0.83	0.00		0.58			0.37			-0.17	
Verify score		0.46					0.27						0.72						0.30	0.93	0.55		0.71			0.82			0.26	
Psi Blast		4.8e-25					6.4e-26						30-21						3.2c-22	1.6e-17	3.2e-16		3e-17			1.5e-16			4.8e-31	
END		216					233						461						208	409	505		417			412			301	
STAR T AA		128					128						331						126	327	127		323	_		321			126	
CHAI N ID		CL.					H						Ξ						<	₹	¥					4				
PDB ID		lovj					lcvj.						lcvj						1d8z	1d8z	1d9a		1jut			1fje			Ihal	
SEQ ID NO:		1700					1700						1700						1700	1700	1700		1700			1700			1700	

	P, RBD,	J. RBD,	J. RBD,	- -	-		
PDB annotation	NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN	NUCLEAR PROTEIN HETRROGARBOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNF, RBD, RRAM, RNF, RNA BINDING, 2 RRAM, RNF, RNA BINDING, 2	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, NNA BINDING, 2 RRM, RNP, TNA BINDING, 2	RNA BINDING PROTEIN RNA- BINDING DOMAIN	RNA BINDING PROTEIN RNA- BINDING DOMAIN		
	N R R	N H N N N N	E H B E H B	BIN BIN	RN/ BIN		
Coumpound		HNRNP AI; CHAIN: NULL;	HNRNP A I; CHAIN: NULL;	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN DO; CHAIN: A;	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN DO; CHAIN: A:	PROPIED FROM US MALL NUCLEAR ROW US SANAL NUCLEAR ROW US SANAL US STATEMANNAL NUS STATEMANNAL WHICH SERBILES I - 95) MUTAN' WITH GLN 8S INRC4 INRC5 STATEMANNAL NUTAN' WITH GLN 8S INRC5 STATEMANNAL NUTA	RIBONUCLEOPROTEIN PROTEIN FROM UI SMALL
SEQFOL D score							
PMF		-0.19	0.99	0.77	96.0	0.49	0.43
Verify score		0.17	0.78	0.82	98.0	-0.09	-0.19
Psi Blast		1.6e-20	1.4e-34	4.8e-23	1.3e-20	1.6e-12	1.36-12
END		405	481	506	399	209	207
STAR		226	325	127	331	127	127
CHAI				¥.	¥	<	м
PDB		IhaI	Ihai	1hd1	1hd1	Inrc	lnrc
SEQ No.		1700	1700	1700	1700	1700	1700

PDB annotation		RIBONUCLEOPROTEIN PTB, PTB- C198, HETEROGENEOUS NUCLEAR POLYPYRIMIDINE TRACT BINDING PROTEIN, RNP, RNA, SPICING, 2 TRANSILATION		COMPLEX (RIBONUCLEOPROTEINRNA)	RNA BINDING PROTEIN RNA- BINDING DOMAIN	RNA-BINDING DOMAIN RNA- BINDING DOMAIN, ALTERNATIVE SPLICING	RNA-BINDING DOMAIN RNA- BINDING DOMAIN, ALTERNATIVE SPLICING	NUCLEAR PROTEIN UI SNRNP A PROTEIN; RNA BINDING DOMAIN,
Coumpound	UI) INRC 3 (N-TERMINAL FRAGMENT, RESIDUES 1 - 95) MUTANT WITH GLN 85 INRC 4 REPLACED BY CYS (Q85C) INRC 5	POLYPYRIMIDINE TRACT- BINDING PROTEIN; CHAIN: A;	RNA-BINDING PROTEIN SEX- ETHAL ROTEIN (C. TERMINUS, OR SECOND RNA- BINDING DOWNEN I SXX. 3 (BRD-2), RESIDICES 199-294 PLUS W-TERMINAL MET) ISXL 4 (NAR, 17 STRUCTURES) ISXL	UIA SPLICEOSOMAL PROTEIN; IURN 5 CIANI: A, B, C; IURN 6 RNA 21MER HAIRPIN (5* (AP*AP*UP*CP*CP*AP*UP*UP* IURN II CHAIN: P, Q, R IURN 13	MUSASHII; CHAIN: A;	SEX-LETHAL PROTBIN; CHAIN: NULL;	SEX-LETHAL PROTEIN; CHAIN: NULL;	UI SMALL NUCLEAR RIBONUCLEOPROTEIN A;
SEQFOL D score								1
PMF		-0.14	0.33	66.0	0.10	0.11	0.84	96'0
Verify		0.25	90:00	0.71	0.59	0.47	0.82	09:0
Psi Blast		4.8e-09	1.4e-15	60-16	3.2e-18	1.3e-20	1.1e-17	4.5e-16
END		217	211	406	206	210	411	406
STAR T AA		128	126	323	127	126	328	322
CHAI N ID		₹		<	٧			
EDB EL		1qm9	Isxi	The state of the s	2mss	2sxi	2sxl	2ula
SEQ NO. ID		1700	1700	1700	1700	1700	1700	1700

TAA	END	Psi Blast	Verify	PMF	SEQFOL D scere	Coumpound	PDB annotation
	-						
						CHAIN: NULL;	NUCLEAR PROTEIN
	206	9.6e-13	0.53	0.05		SPLICING FACTOR UZAF 65 KD SUBUNIT; CHAIN: A;	RNA-BINDING PROTEIN SPLICING, U2 SNRNP, RBD, RNA-BINDING PROTEIN
	311	1.1e-34	0.01	-0.19		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	COMPLEX (RIBONUCLEOPROTEINDNA) HNRNP AI, UPI; COMELEX (RIBONUCLEOPROTEINDNA), HEITEROGENEOUS NUCLEAR 2 PROMETER 2
	410	4.8c-22	0.35	-0.14		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DIVA; CHAIN: B;	COMPLEX COMPLEX COMPLEX (RIBONUCLEOPROCIBEINDAA) HNRNR AI, UPI; COMPLEX (RIBONUCLEOPROCIBEINDAA), HFTERGORIBOUS NUCLEAR 2 PROVINCE ROBEOTEN AI
	484	1.3e-35	0.49	0.87		HETEROGENBOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	COMPLEX (CRIBON/CLEOPROTEIN/DNA) HNRNP A1, UP1; COMPLEX (RIBONI/CLEOPROTEIN/DNA), HETIROGENBOUS NUCLEAR 2 RIBONICLEOPROTEIN A1
	474	3.26-29	1.01	1.00		SEX-LETHAL; CHAIN: A, B, C;	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA BECONNTION MOTTE, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX.3 BENERALITATIONAL INHIBITOR, SEX.3 DETERMINATION, X CERCOMOSOME DOSAGE COMPENSATION
	161	4.5e-30			92.79	TUMOR SUPPRESSOR PIGINK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
	298	3e-45	0.92	1.00		GA BINDING PROTEIN ALPHA; COMPLEX (TRANSCRIPTION	COMPLEX (TRANSCRIPTION

PDB annotation	REGULATION/DNA) GABPALPHA; GABBETAL; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING,	2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	GOMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETAI: COMPLEX	(TRANSCRIPTION REGULATIONDINA), DNA-BINDING,	2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS,	+	REGULATION/DNA) GABPALPHA; GABPBETA1: COMPLEX	(TRANSCRIPTION	REGULATION/DNA), DNA-BINDING,	ANKYRIN REPEATS,	F	_	GABPBETAI; COMPLEX	REGULATION/DNA), DNA-BINDING,	2 NUCLEAR PROTEIN, ETS DOMAIN,	ANKYRIN REPEATS,	+-	REGULATION/DNA) GABPALPHA; GABPBETA1-COMPLEX
Coumpound	CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B;	DNA; CHAIN: D, E;		GA BINDING PROTEIN ALPHA;	PROTEIN BETA I; CHAIN: B;	DNA; CHAIN: D, E;			GA BINDING PROTEIN ALPHA:	CHAIN: A; GA BINDING	PROTEIN BETA I; CHAIN: B;	לה לה יוווים להווים			GA BINDING PROTEIN ALPHA;	CHAIN: A; GA BINDING PROTEIN BETA 1: CHAIN: B:
SEQFOL D score																	90.41	
PMF			1.00			1.00					1.00							
Verify score			0.94			06.0					1111							
Psi Blast			1.1e-40			30-39					1.6e-37						3e-45	
END			298			165					165						363	
STAR T AA			120			15		_			17						212	
CHAI N ID			æ			В					В						m	
FDB ID			lawc			lawc					Iawc						lawc	
SEQ ID NO:			1701			1701					10/1						1701	

	DING, MAIN,	HA; DING, MAIN,	HA; DING, MAIN,	HA; DING, MAIN,	HA;
ation	DNA-BIN 4, ETS DO ACTOR	GABPALI GABPALI EX DNA-BIN 4, ETS DO	GABPALF GABPALF EX DNA-BIN 4, ETS DO	GABPALE EX DNA-BIN 4, ETS DO	SABPALE EX
PDB annotation	PTION ON/DNA), PROTEIN EPEATS, TION 3 F	TRANSCI NVDNA) 1; COMPI PTION NVDNA), PROTEI EPEATS,	TRANSCI II, COMPI PTION PROTEI PROTEI EPEATS,	TRANSCI NVDNA) I; COMPI PTION NVDNA), PROTEIN EPEATS,	TRANSCI NVDNA) I; COMPI TION
	(TRANSCRIPTION REGULATIONDNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION REGULA TROMDA) GABRALPHA; GABRIETAI; COMPLEX (TRANSCREPTION) ESCULATIONODAA), DAA-BINDING, S NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 PACTOR	COMPLEX (TRANSCRIPTION REGULATION/DAY) GABRALPHA; GARBERTAI; COMPLEX (TRANSCREPTION) REGULATION/DAY) DAY-BINDING, STOUCHEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 PACTOR	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABRALPHA; GARBERTAL; COMPLEX (TRANSCREPTION) REGULATION/DNA), DNA-BINDING, STOUCLAR PROTEIN, ETS DOMAIN; ANKYRIN REPEATS, TRANSCREPTION 3 PACTOR	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA; COMPLEX (TRANSCRIPTION PEGII ATTOM/DNA) THA BENERIC
		L.PHA;	LPHA;	LPHA;	₹
Coumpound	ii i	ROTEIN A	ROTEIN A	ROTEIN A	ROTEIN A SINDING 1; CHAIN
Coun	DNA; CHAIN: D, B;	GA BINDING PROTEIN ALPHA; CARIN A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D; E;	GA BINDING PROTEIN ALPHA; CANIN A; CB BINDING PROTEIN B; CHAIN: B; DNA; CHAIN: D; E;	GA BINDING PROTEIN ALPHA; CANDIN A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E;	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;
	DNA;	GA BI CHAII PROTI DNA;	GA BI CHAID PROTI DNA;	GA BI CHAR PROTI DNA;	GA BI CHAID PROTI DINA;
SEQFOL D score					
PMF		1.00	1.00	1.00	1.00
Verify score		0.64	0.25	1.07	0.46
Psi Blast		1.2e-41	3.2e-32	Ie-32	6e-39
END		395	427	405	8
STAR		212	250	278	45
CBAI N ID		g;	æ	я	E E
PDB ID		lawc	lawc	lawc	Iawc
SEQ NO. 13		1701	1701	1701	1701

	S DOMAIN,	ON ALPHA;	BINDING, S DOMAIN,	JR.	MOR IIBITOR,	MOR. IIBITOR,	MOR	IIBITOR,	MOR	IIBITOR,	MOR	ilbii Ok,	MOR	in Dillor,	MOR	IIBTIOK,	MOR
PDB annotation	2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX	(TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS,	TRANSCRIPTION 3 FACTOR	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTTE	TUMOR SUPPRESSOR TUMOR	SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR	SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR	SOFTIESSOR, CDAR'S INHIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR	ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR	SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR CDK4/6 INHIBITOR
Coumpound	7.4	EIN ALPHA; DING CHAIN: B;	DNA; CHAIN: D, E;	7	P19INK4D CDK4/6 INHIBITOR; 1 CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; T CHAIN: NULL; S	4/6 INHIBITOR;	CHAIN: NULL;	:4/6 INHIBITOR;	CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; T		P19INK4D CDK4/6 INHIBITOR; 1		:4/6 INHIBITOR;	CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; T
SEQFOL D score						87.58											
PMF		1.00			1.00		1.00		1.00		0.77		1.00		1.00		1.00
Verify		0.72			0.42		0.85		0.81		65.0		0.67		0.44		08.0
Psi Blast		4.8c-37			3e-37	1.4c-38	7.5e-38		1.5e-37		1.4e-38		4.5e-30		1.4e-36		I.4e-38
END		661			299	301	168		333		397		405		201		234
STAR T AA		20			113	145	17		183		215		279		46		82
CHAI N ID		В															
an OI		lawc			Ibd8	1bd8	1bd8		1bd8		1bd8		1bd8		1bd8		15d8
SEQ ID NO:		1701			1701	1701	1701		1701		10/1		1701		1701		1701

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PDB annotation	ANKYRIN MOTIF	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN CYCI IN-DEPENDENT	KINASE, CELL CYCLE 2 CONTROL,	ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR	PROTEIN/KINASE) INHIBITOR	PROTEIN, CYCLIN-DEPENDENT	ALPHA/BETA, COMPLEX	(INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR	PROTEIN/KINASE) INHIBITOR	PROTEIN, CYCLIN-DEPENDENT	KINASE, CELL CYCLE 2 CONTROL,	ALPHA/BETA, COMPLEX	(INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR	PROTEIN, CYCLIN-DEPENDENT	KINASE, CELL CYCLE 2 CONTROL,	ALPHA/BETA, COMPLEX	(INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR	PROTEIN/KINASE) INHIBITOR	PROTEIN, CYCLIN-DEPENDENT	KINASE, CELL CYCLE 2 CONTROL,	ALPHA/BETA, COMPLEX	(INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR	PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT
Coumpound		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B:	î		CYCLIN-DEPENDENT KINASE	6; CHAIN: A; P19INK4D; CHAIN:	÷,			CYCLIN-DEPENDENT KINASE	6; CHAIN: A; P19INK4D; CHAIN:	à				CYCLIN-DEPENDENT KINASE 6: CHAIN: A: P19INK4D: CHAIN:	Ď				CYCLIN-DEPENDENT KINASE	6; CHAIN: A; P19INK4D; CHAIN:	B;				CYCLIN-DEPENDENT KINASE	6; CHAIN: A; P19INK4D; CHAIN: B;
SEQFOL D score					80.38																							
PMF		1.00								1.00						0.1					1.00						1.00	
Verify		0.72								0.92						0.48					0.43						0.32	
Psi Blast		9e-38			1.5e-39					1.5e-39						1.4e-38					3e-39						96-38	
END		271			170					170						338					401						205	
STAR T AA		114			12					13							_				215						9	
CHAI N ID		Д			В					д						Д					ф						Д	
PDB CI		1blx			1bk					1blx						16lx					1blx						10lx	
SEQ NO:		1701			1701					1201						1701					1701						1701	

PDB annotation	KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	HORMONE/GROWTH FACTOR P18-	P18INK4C, TUMOR, SUPPRESSOR,	CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR	HORMONE/GROWTH FACTOR P18-	PISINK4C, TUMOR, SUPPRESSOR.	CYCLIN- 2 DEPENDENT KINASE,	HORMONE/GROW I'H FACTOR	SIGNALING PROTEIN HELIX-TURN- HELIX ANKYRIN REPEAT	SIGNALING PROTEIN HELIX-TURN-	HELIX, ANKYRIN REPEAT	CELL CYCLE INHIBITOR P18-	INK4C(INK6); CELL CYCLE	INHIBITOR, P18-INK4C(INK6),	ANKYRIN REPEAT, 2 CDK 4/6	INHIBITOR	CELL CYCLE INHIBITOR P18-	INK4C(INK6); CELL CYCLE	INHIBITOR, P18-INK4C(INK6),	ANKYRIN REPEAT, 2 CDK 4/6	INHIBITIOR	TRANSCRIPTION FACTOR P65;	P50D; TRANSCRIPTION FACTOR,	IKB/NFKB COMPLEX		TRANSCRIPTION FACTOR P65;	P50D; TRANSCRIPTION FACTOR,	IKB/NFKB COMPLEX
Coumpound		CYCLIN-DEPENDENT KINASE 6 INHIBITOR: CHAIN: A:			CYCLIN-DEPENDENT KINASE	OHNIMBHON, CHAIN. A,			CYCLIN-DEPENDENT KINASE 4 INHIBITOR B: CHAIN: A:	CYCLIN-DEPENDENT KINASE	4 INHIBITOR B; CHAIN: A;	CYCLIN-DEPENDENT KINASE	6 INHIBITOR; CHAIN: A, B;				CYCLIN-DEPENDENT KINASE	6 INHIBITOR; CHAIN: A, B;				NF-KAPPA-B P65 SUBUNIT;	CHAIN: A; NF-KAPPA-B P50D	SUBUNIT; CHAIN: C; I-KAPPA-	B-ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT;	CHAIN: A; NF-KAPPA-B P50D	SUBUNIT; CHAIN: C; 1-KAPPA-
SEQFOL D score					92.05												89.22											
PMF		0.25							96.1	1.00		0.93										0.35				1.00		
Verify		0.24							0.60	0.80		0.43										0.19				0.71		
Psi Blast		3.2e-30			1.3e-35				3e-37	1.5e-36		1.4e-29					9e-38					1.2e-53				1.5e-39		
END		432			177				757	104		431					236					371				173		
STAR T AA		253			6				104	269		253					28					145				17		
CHAI N ID		V			V				۷	V		V					٧					Ω				Ω		
EDB OI		1bu9			1bu9				SKDI	149s		lihb				-	1Hb					ii B				Ē		
SEQ ID NO:		1701			1701				10/1	1701		1701					1701					1701				1701		

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PDB annotation		TRANSCRIPTION FACTOR P65;	P50D; TRANSCRIPTION FACTOR,	IKB/NFKB COMPLEX	THE ASSOCIATION IS A COLOR DOCK.	TRANSCRIPTION FACTOR P65;	P50D; TRANSCRIPTION FACTOR,	IKB/NFKB COMPLEX	TRANSCRIPTION FACTOR P65;	P50D; TRANSCRIPTION FACTOR,	IKB/NFKB COMPLEX	as a mount of a community of the same	IKANSCRIPTION FACTOR Pos;	P50D; TRANSCRIPTION FACTOR,	IKB/NFKB COMPLEX		TRANSCRIPTION FACTOR P65;	P50D; TRANSCRIPTION FACTOR,	IKB/NFKB COMPLEX		TRANSCRIPTION FACTOR P65;	P50D; TRANSCRIPTION FACTOR,	IKB/NFKB COMPLEX		ANK-REPEAT MYOTROPHIN,	ACETYLATION, NMR, ANK-REPEAT	COMPLEX (TRANSCRIPTION	REG/ANK REPEAT) COMPLEX	(TRANSCRIPTION	REGULATION/ANK REPEAT),	ANKYRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX
Coumpound	B-ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT;	CHAIN: A; NF-KAPPA-B P50D	SUBUNIT; CHAIN: C; I-KAPPA-	NE VARIA DING CIRING	NF-KAPPA-B P65 SUBUNIT	CHAIN: A; NF-KAPPA-B P50D	SUBUNIT; CHAIN: C; I-KAPPA- B-AI PHA: CHAIN: D:	NF-KAPPA-B P65 SUBUNIT:	CHAIN: A; NF-KAPPA-B P50D	SUBUNIT; CHAIN: C; I-KAPPA-	B-ALPHA, CHAIN: D;	Nr-KAPPA-B POS SUBUNIT;	CHAIN: A; NF-KAPPA-B P50D	SUBUNIT; CHAIN; C; I-KAPPA-	B-ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT;	CHAIN: A; NF-KAPPA-B P50D	SUBUNIT; CHAIN: C; I-KAPPA-	B-ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT;	CHAIN: A; NF-KAPPA-B P50D	SUBUNIT; CHAIN: C; 1-KAPPA-	B-ALPHA; CHAIN: D;	MYOTROPHIN; CHAIN: NULL		NF-KAPPA-B P65; CHAIN: A, C;	NF-KAPPA-B P50; CHAIN: B, D;	I-KAPPA-B-ALPHA; CHAIN: E,	ė.		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D;
SEQFOL D score																	81.35	_														
PMF		0.92			800	8			1.00			8	1.00								0.99				0.71		00.					0.99
Verify		0.05			070	0.49			0.11				0.13								0.28				0.26		95.0					0.10
Psi Blast		1.1e-38			30.60	26-50			4.8e-43			00	4.30-32				4.5e-52				4.5e-52				1.5e-30		96-51					3e-49
END		427			400	403			232			9,0	0+7				253				276				391		311					401
STAR T AA		212	_		316	C12			45			100	5				45				82		_		247		113					143
CHAI		۵			-	_			D			-	_				Д				۵						ш					В
PDB DD		- Ika			11111		_		likn			11.	IKU				liku				ä	_			lmyo		yı		_			lnfi
SEQ No D		1701			1201	10/1			1701			1701	5				1701				1701				1701		1701					1701

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PDB annotation	(TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION REGANK REPEAT) COMPLEX TRANSCRIPTION REGULATION/ANK REPEAT), ANK YRIN 2 REPEAT HELLX	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANK YRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANK YRN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANK YRN 2 REPEAT HEI IX	COMPLEX (TRANSCRIPTION REGIANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANK YRM 2 REPEAT HELIX	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ANKYRIN REPEATS, CRITCYCLE	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ANKYRIN REPEATS, CELL-CYCLE
Coumpound	I-KAPPA-B-ALPHA; CHAIN: E, F;	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: B, F;	NF-KAPPA-B P65, CHAIN: A, C, NF-KAPPA-B P50; CHAIN: B, D; FKAPPA-B-ALPHA; CHAIN: B, F;	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: B, F;	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; F-KAPPA-B-ALPHA; CHAIN: B, F;	REGULATORY PROTEIN SWI6; CHAIN: A, B;	REGULATORY PROTEIN SWIG; CHAIN: A, B;
SEQFOL D score				87.55				70.20
PMF		0.1	0.70		1.00	00.1	0.28	
Verify		0.94	0.42		0.50	0.59	-0.06	
Psi Blast		4.5e-39	1.10-38	1.5e-51	1.5e-51	6.4e-43	4.5e-36	4.50-36
END		170	427	242	238	232	287	320
STAR T AA		17	210	42	43	4	19	76
CHAI N ID		m	ш	ш	ш	ய	∢	∢
PDB CII		gu g	Infi	gu 1	gui	Infl	1sw6	1sw6
S e S		1701	1701	1701	1701	1701	1701	1701

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PDB annotation	ONCOGENEZA (ARTICLE) PSTREY, ANK TRIN REPEATS, SHY, PSTREY, ANK TRIN REPEATS, SHY, MULTIGENES PRAMITY, MUCLEAR, MULTIGENES PRAMITY, MUCHEAR, PSTREY,	ONCOREDE (ANT) PSTREY, ANNYRIN REPEATS, SHI, PSTREY, ANNYRIN REPEATS, SHI, PSTREY, ANNYRIN REPEATS, SHI, MULTIGENE STAMITY, MOCLEAR, MULTIGENE PRAMITY, MOCLEAR, DISTAS, BAUTATION, 3 PSTREAS, BAUTATION, 3 ONCOGNICATION, 3	KINASE KINASE, SIGNAL TRANSDUCTION,	CALLIONICALMODOLIN	CYCLIN-DEPENDENT PROTEIN PROTEIN KINASE CDK2; PROTEIN
Coumpound	953; CHAIN: A; 53BP2; CHAIN: B;	PS3, CHAIN: A; 53BP2, CHAIN: B;	CALCTUM/CALMODULIN- DEPENDENT PROTEIN KINASE;	CHARLE WILL OF THE ALL ALL ALL ALL ALL ALL ALL ALL ALL AL	CYCLIN-DEPENDENT PROTEIN
SEQFOL D score	70.78				
PMF		0.55	0.65	0.86	0.11
Verify		-0.07	80.0	0.30	0.22
Psi Blast	7.5e-35	4.5e-37	1.6e-70	6.4e-98	1.1c-46
END AA	396	283	303	312	266
STAR T AA	214	81	31	23	29
CHAI N ID	м	æ		ш	
PDB	1yes	1yes	1a06	lapm	ladl
SEQ NO:	1701	1701	1702	1702	1702

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PDB annotation	KINASE, CELL CYCLE, PHOSPHORYLATION, STAUROSPORINE, 2 CELL DIVISION, MITOSIS, INHIBITION	SCAFFOLD PROTEIN SCAFFOLD PROTEIN, PP2A, PHOSPHORYLATION, HEAT REPEAT	SCAFFOLD PROTEIN SCAFFOLD PROTEIN, PP2A, PHOSPHORYLATION, HEAT REPEAT			TRANSFERASE KINASE DOMAIN, AUTOINHIBITORY FRAGMENT, HOMODIMER	PROTEIN KINASE CDK2; TRANSREASAS, SERNETIREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION	NUCLEAR IMPORT RECEPTOR KARYOPHERIN ALPHA; NUCLEAR IMPORT RECEPTOR, NUCLEAR LOCALIZATION SIGNAL, 2
Coumpound	KINASE 2; CHAIN: NULL;	PROTEIN PHOSPHATASE PP2A; CHAIN: A, B;	PROTEIN PHOSPHATASE PP2A; CHAIN: A, B;	PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT ICMK 3 (E.C.2.7.1.37) ICMK 4	TRANSFERASE(PHOSPHOTRA NSFERASE) CAMP. DEPENDENT PROTEIN KINASE (E.C.27.1.37) (CAPK) 1CTP 3 (CATALYTIC SUBUNIT) 1CTP 4	SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: A, B; SERINE/THREONINE- PROTEIN KINASE PAK-ALPHA; CHAIN: C, D;	HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	IMPORTIN ALPHA; CHAIN: A;
SEQFOL D score								
PMF		00.1	1.00	0.75	0.86	0.98	0.60	0.24
Verify score		0.22	0.29	0.10	0.01	0.35	0.26	0.26
Psi Blast		0.0003	1.4e-33	3.2e-99	8e-94	3.2e-49	4.8c-49	6e-05
END		416	260	312	303	264	266	551
STAR T AA		231	278	29	29	29	58	328
CHAI N ID		٧	4	E	Э	S		∢
PDB CII		Ib3u	Ib3u	1cmk	letp	If3m	Ihel	E
SEQ ID NO:		1702	1702	1702	1702	1702	1702	1702

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PDB annotation	ARMADILLO REPEATS, AUTOINHIBITION, INTRASTERIC REGULATION	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE; TRANSFERASE, MAP KINASE, SERINE/THREONINE-PROTEIN KINASE, 2 P38	KINASE RABIT MUSCLE PHOSPHOYYLASE KINASE; GLYCOGEN METABOLISM, ITRANSFIRASE; SERINETHREONINE-PROTEIN, 2 KINASE, ATP-BINDING,	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEMPEPTIDE)	STRUCTURAL PROTEIN ARMADILLO REPEAT, BETA- CATENIN, STRUCTURAL, PROTEIN	CALCIUM-BINDING PROTEIN CALCIUM-MYRISTOYL SWITCH, CALCUIM-BINDING PROTEIN	CELL CYCLE REGULATION CELL CYCLE REGULATION, HERPESVIRUS SAIMIRI, VIRAL
Coumpound		TWITCHIN; CHAIN; NULL;	TWITCHIN; CHAIN: A, B;	MAP KINASE P38, CHAIN: NULL;	PHOSPHORYTASE KINASE; CHAIN: NULL;	CALMODULIN; CHAIN: A; RS20; CHAIN: B;	BETA-CATENIN; CHAIN: NULL;	RECOVERIN; CHAIN: NULL;	CYCLIN HOMOLOG; CHAIN: A;
SEQFOL D score				81.88					
PMF		0.75	96'0		66:0	60'0	0.52	0.07	0.30
Verify		0.30	0.51		0.48	0.18	-0.31	-0.04	-0.26
Psi Blast		1.3e-58	8c-57	3.2e-42	6.4e-71	1.1e-19	0.0001	0.0003	3.2e-26
END AA		304	265	334	264	453	260	440	352
STAR T AA		29	29	es.	31	301	438	308	157
CHAI N ID			∀			¥			4
PDB ID		1koa	Ikob	1p38	Iphk	lvrk	2bct	Iika	1bu2
SEQ NO:		1702	1702	1702	1702	1702	1702	1704	1705

PDB annotation	CYCLIN	TRANSCRIPTOR NUTLATION TRANSCRIPTOR NUTLATION TRANSCRIPTOR NUTLATION FACTOR IN THAT SEQUENCE BINDING PROTEIN PROTEIN-DIA BINDING PROTEIN, PROTEIN-DIA HELK-TURA-HELK, 2 1717BOX, TRANSCRIPTION/DNA	COMPLEX (PROTEIN FINASECYCLIN) CYCLIN- BEPENDENT KIRASE2, CDK2, P33 PROTEIN KIRASE, CCN4, CCN1; COMPLEX (PROTEIN CONF.) KINASECYCLIN), CYCLIN, CDK, 2 PHOSPHORYLATION, SUBSTRATE	BINDING PROTEIN CYCLIN, CELL CYCLE, KINASE-REGULATORY-SUBUNIT, 2 BINDING PROTEIN	TRANSCRIPTION INHIBITOR BETA- PROPELLER	COMPLEX (GTP. BRYDINGTRANSDICER) BETA1, TRANSDICTN BETA SUBUNIT; TRANSDICTN BETA SUBUNIT; TRANSDICTN GAMMA SUBUNIT; COMPLEX (GTP. BINDINGTRANSDICER), G PROTEN, HETREOTRANER 2
Coumpound		GORDERAL TRANSCRIPTION FACTOR IB: GTANE A.E. I. M. QC, TATA BORE BINDING PROTEIN: GHAIN: B.F. J. N.R. ADMLP TATA-BOX DIVA CONTAINING IIB RECOGNITION GEARINE, C, G, K, GO, SI, ADMLP TATA-BOX DIVA CONTAINING IIB RECOGNITION GEARINE, C, M. ERCOGNITION GEARINE, C, M. FRECOGNITION GEARINE, D, H. J. P. T.	KINASE Z. CHANIN, ROCELD PAYSION PROTEIN KINASE Z. CHANIN, A, C, CZAMITOTIC-SPECIFIC CYCLIN A; CHANIN, B, F; PEPTIDE; CHAIN; B, F;	CYCLIN A; CHAIN: NULL;	TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;	GT-AI PHA/GI-AI PHA CHIMERA; CHAIN: A; GT- BETA; CHAIN: B; GT-GAMMA; CHAIN: G;
SEQFOL D score						
PMF		0.17	0.01	0.04	1.00	0.93
Verify		-0.02	-0.21	-0.11	0.65	0.35
Psi Blast		1.3e-23	4.8e-49	4.8e-48	8e-67	1.4e-59
END		350	345	345	571	529
STAR T AA		183	136	142	277	230
CHAI N ID		¥	m .		Ą	m
PDB ID		1c9b	Iqmz	lvin	1erj	Igot
SEQ ID NO:		1705	1705	1705	1708	1708

PDB annotation	SIGNAL TRANSDUCTION	COMPLEX (CITP. BINDING/TRANSDUCER) BETA1, TRANSDUCIN BETA SUBUNT; GAMMA, TRANSDUCIN GAMAA SUBUNT; CONFLEX (CITP. BINDING/TRANSDUCER), G ROTER, HETBEGTTANKE 2 SIGNAL TRANSDUCTIONE ROTER TRANSDUCTION ROTER	COMPLEX (GTP. BINDING/TRANSDUCER,) BETA1, TRANSDUCIN BETA SUBUNT; GAMMAI, TRANSDUCIN GAMMA SUBUNT; COMPLEX (GTP. BINDING/TRANSDUCER), G PROTEIN, HETEOTRUMER 2 RGGAAL, TRANSDUCTION	COMPLEX (TRANSFERASE/FEPTIDE) COMPLEX (TRANSFERASE/FEPTIDE)		COMPLEX (PROTO- ONCOGENEEARLY PROTEIN) SRC HOMOLOGY 2 DOMAIN; SH2 DOMAIN, SIGNAL TRANSDUCTION.
Coumpound	The same and the s	GT-ALPHAOG-ALPHA GHAIREA, CHAIN: A; GT- BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	GT-AIPHAOI-AIPHA CHAIREA; CHAIN: A; GT- BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	C-SRC TYROSINE KINASE; CHAIN: A, B; ACE-FORMYL PHOSPHOTYR-GLU-(N,IN- DIPENTYL AMINE); CHAIN: C, D:	TRANSFERASE/PHOSPHOTRA NSFERASE) PROTO- ONCOGENE TYROSINE KINASE (E.C.7.1.112) IAB2 3 (SRC HOMOLOGY 2 DOMAIN) (ABELSON, SITS ABL) IAB2 4 (NMR. 20 STRUCTURES) IAB2 4	FYN PROTEIN-TYROSINE KINASE; CHAIN: F; PHOSPHOTYROSYI, PEPTIDE; CHAIN: P
SEQFOL D score		104.96				
PMF			1.00	0.09	0.12	0.06
Verify			0.55	0.56	0.38	0.47
Psi Blast		I.6e-69	1.6e-69	8e-25	1.6e-22	4.8e-21
END		269	569	380	382	378
STAR T AA		242	280	282	282	282
CHAI		м	g B	∢		gs.
PDB ED		1got	1got	1a09	lab2	laot
SEQ NO B		1708	1708	1709	1709	1709

PDB annotation	PEPTIDE COMPLEX, 2 COMPLEX (PROTO-ONCOGENE/EARLY PROTEIN)	ASE V-SRC SH2 DOMAIN SRC SH2; V-SRC SH2 DOMAIN, PHOSPHOTYPOSINE RECOGNITION DOMAIN PROF SRC SH2 DOMAIN					COMPLEX (KINASE/PEPTIDE)	COMPLEX (TYROSINE KINASE/PEPTIDE)
Coumpound		PP60 V-SRC TYROSINE KINASE TRANSFORMING PROTEIN; CHAIN: NULL;	P55 BLK PROTEIN TYROSINE KINASE; CHAIN: NULL;	SYK PROTEIN TYROSINE KINASE, CHAIN: A; ACETYL- THR-PTR-GLU-THR-LEU-NH2; CHAIN: B;	P56LCK TYROSINE KINASE; CHAIN: L; PHOSPHONOPEPTIDE CHAIN: P:	GROWTH FACTOR RECEPTOR BOUND PROTEIN-2; CHAIN: NULL;	P56==LCK== TYROSINE KINASE; ILCK 7 CHAIN: A; ILCK 8 TAIL PHOSPHOPEPTIDE TEGQPHOSPHOYQPQPA; ILCK 14 CHAIN: B: ILCK 15	HUMAN PS6 TYRÓSINE KINASE, ILKK 7 CHAIN: A; ILKK 8 PHOSPHOTYROSYL PEPTIDE AC-PTYR-GLU-GLU- II PEPTIDE AC-PTYR-GLU-GLU-GLU-GLU-GLU-GLU-GLU-GLU-GLU-GLU
SEQFOL D score								
PMF		0.01	0.07	-0.01	0.07	0.16	0.01	0.15
Verify		0.29	0.31	0.44	0.13	0.18	0.08	0.49
Psi Blast		1.6e-24	1.6e-22	1.16-17	1.4e-19	1.1e-17	6.4e-26	3.2e-21
END		385	379	379	375	377	379	379
STAR T AA		284	275	281	286	281	242	282
CHAI N ID				<	ı		٧	∀
PDB ID		1981	<u>1</u> 2	losy	1cwd	1fhs	11ck	IIKk
SEQ ID NO:		60/1	1709	1709	1709	1709	1709	6021

PDB annotation				TYROSINE PHOSPHATASE SYP, SHPTP-2; TYROSINE PHOSPHATASE, INSULIN SIGNALING, SH2 PROTEIN	TRANSFERASE HCK, SH2, TYROSINE KINASE, SIGNAL TRANSDUCTION, TRANSFERASE	HALOPEROXIDASE BROMOPEROXIDASE 1, HALOPEROXIDASE 1, HALOPEROXIDASE 1, OXIDORENI OXIDASE 1, OXIDORENI OXIDASE 1,	HALOPEROXIDASE BROMOPEROXIDASE L, HALOPEROXIDASE L; HALOPEROXIDASE,
Coumpound	12	PHOSPHOTRANSFERASE V. SRC TYROSINE KINASE TRANSFORMING PROTEIN (PHOSPHOTYROSINE 1518 A 3 RECOGNITION DOMBEX WITH STRA 4 PROSPHOEPTIDE A (TYR-VAL-PRO-MET-LEU, PHOSPHORYLATED TYR) 15HA	SIGNALLING PROTEIN PHOSPHATIDYLINGSITOL 3- KINASE (E.C.Z.I.137) (N- TERMINAL ZPRA 3 SHZ DOMAIN OF P85-ALPHA SUBUNIT) (NMR, 22 SUBUNIT) (NMR, 22	SHP-2; CHAIN: A, B;	HCK SH2; CHAIN: NULL;	CHLOROPEROXIDASE L; CHAIN: A, B, C;	CHLOROPEROXIDASE L; CHAIN: A, B, C;
SEQFOL D score						85.13	
PMF		0.07	0.78	0.04	0.25		1.00
Verify		0.51	0.33	-0.31	0.19		0.36
Psi Blast		1.6e-24	6.4e-18	3.2e-27	1.6e-22	3e-41	3e-41
END		380	383	439	379	357	356
STAR T AA		284	286	257	281	76	26
CHAI N ID		∢		A		<	4
PDB UD		1sha	2pne	2shp	3hck	1a88	1a88
SEQ ID NO:		1709	1709	1709	1709	1710	1710

	OXIDOREDUCTASE		HALOPEROXIDASE AI;		HALOPEROXIDASE F;	OXIDOREDUCTASE, PROPIONATE	SE F; HALOPEROXIDASE	TIAL OPER CATE ASE F;	OXIDOREDICTASE PROPIONATE	COMPLEX		AMINOPEPTIDASE, PROLINE	IMINOPEPTIDASE, SERINE	PROTEASE, 2 XANTHOMONAS	CAMPESTRIS		HAIN: HALOALKANE DEHALOGENASE,	HANDOT AST HANDA AST			ľ	HALOPEROXIDASE A2,	CHLOROPEROXIDASE A2;	HALOPEROXIDASE,	OXIDOREDUCTASE, PEROXIDASE,	
Coumpound		BROMOPEROXIDASE AI; CHAIN: NULL;		CHLOROPEROXIDASE F;	CHAIN: NULL;		CHLOROPEROXIDASE F;	CHAIN, NOLL,			PROLINE IMINOPEPTIDASE;	CHAIN: A, B;				HALOALKANE	DEHALOGENASE; CHAIN:	DALOALVANE	DEHAI OGENASE: CHAIN:	NULL:	BROMOPEROXIDASE A2;	CHAIN: NULL;				
SEQFOL D score		95.47		83.84							67.83					94.11					98.68					
PMF score							00'1											1 00	3							
Verify							19:0									_		0.45	}							
Psi Blast		8e-31		9e-41			96-41				I.5e-36		_			3e-43		30.43	7		8e-32					
END		998		357			356				355					357		356	3		357					
STAR		7.8		28			84				83				1	44		83			9/					_
CHAI N ID											4															
EDB EDB		Ia8q		la8s			lags				lazw				1	2001	_	1669	0		1brt					_
SEQ NO:		1710		1710			1710				1710				0.00	01/1		1710			1710					

PDB annotation	HYDROLASE BPHD; HYDROLASE, PCB DEGRADATION	HYDROLASE A/B HYDROLASE FOLD, DEHALOGENASE I-S BOND	HYDROLASE A/B HYDROLASE FOLD, DEHALOGENASE I-S BOND	HYDROLASE LINU, 1,3,4,6- TETRACHORO-1,4- CYCLOHEXADIENE DEHALOGENASE, LINDANE; BIODEGRADATION, ALPHA/BETA- HYDROLASE	HYDROJASE TRIACYLGLYGEROJ- HYDROLASE, XARA CRYSTALLOGRAPHY, 2 PSEUDOMONADACEAE, OXYANION, CIS-PEPTIDE, HYDROLASE	HYDROLASE TRIACYLGLYCEROL HYDROLASE, XARA CRYSTALLOGRAPHY, 2 PSEUDOMONADACCAE, OXYANION, CIS-PEPTIDE, HYDROLASE	HYDROLASE HYDROLASE, ALPHA/BETA HYDROLASE FOLD, EPOXIDE DEGRADATION, 2 EPICHLOROHYDRIN	HYDROLASE HOMODIMER, ALPHA/BETA HYDROLASE FOLD, DISUBSTITUTED UREA 2 INHIBITOR
Coumpound	2-HYDROXY-6-OXO-6- PHENYLHEXA-2,4-DIENOATE CHAIN: A;	HALOALKANE DEHALOGENASE; 1- CHLOROHEXANE CHAIN: A;	HALOALKANE DEHALOGENASE; 1- CHLOROHEXANE CHAIN: A;	HALOALKANE DEHALOGENASE; CHAIN: A;	TRACYLGI YGEROL HYDROLASE, CHAIN: NULL;	TRIACYLGI.YCEROL HYDROLASB; CHAIN: NULL;	SOLUBLE EPOXIDE HYDROLASE; CHAIN: A, B, C, D;	EPOXIDE HYDROLASE; CHAIN: A, B;
SEQFOL D score	77.34	122.01					119.90	
PMF			1.00	1.00	0.63	0.07		1.00
Verify			0.58	0.60	0.11	0.25		0.52
Psi Blast	3.2e-36	9c-47	90-47	3e-44	30-13	4.8c-09	9.6e-37	8e-43
END	357	360	358	358	196	212	356	356
STAR T AA	72	67	74	73	101	25	99	62
CHAI N ID	<	V	A	⋖			∢	V V
EDB EID	lo4x	1cqw	loqw	lev2	lovi	lcvl	lehy	1ck1
SEQ NO:	1710	1710	1710	1710	1710	1710	1710	1710

PDB annotation	HYDROLASE HOMODIMER, ALPHA/BETA HYDROLASE FOLD, DISUBSTITUTED UREA 2 INHIBITOR	HYDROLASE HOMODIMER, ALPHA/BETA HYDROLASE FOLD, DISUBSTITUTED UREA 2 INHIBITOR	HYDROLASE HOMODIMER, ALPHA/BETA HYDROLASE FOLD, DISUBSTITUTED UREA 2 INHIBITOR	HYDROLASE LIPASE	HYDROLASE PNB ESTERASE; ALPHA-BETA HYDROLASE DIRECTED EVOLUTION	HYDROLASE PSEUDOMONADACEAE, CIS- PEPTIDE, CLOSED	CONFORMATION, 2 HYDROLASE, LID	HYDROLASE PSEUDOMONADACEAE, CIS- PEPTIDE, CLOSED PONFORMATION, 2 HYDROLASE, LID	EPOXIDE HYDROLASE EH; EPOXIDE HYDROLASE, ALPHABETA HYDROLASE	HYDROLASE ALPHA BETA HYDROLASE FOLD, PROLINE, PROLYL AMINOPEPTIDASE, 2 SERRATIA, IMNOPEPTIDASE	LIPASE LIPASE; LIPASE, HYDROLASE, PSEUDOMONADACEAE, COVALENT INTERMEDIATE, 2 TRIGLYCERIDE
Coumpound	EPOXIDE HYDROLASE; CHAIN: A, B;	EPOXIDE HYDROLASE; CHAIN: HYDROLASE HOMODIMER, A, B; DISUBSTITUTED UREA 2 INI	EPOXIDE HYDROLASE; CHAIN: A, B;	LIPASE, GASTRIC; CHAIN: A, B;	PARA-NITROBENZYL ESTERASE; CHAIN: A;	TRIACYLGLYCEROL HYDROLASE; CHAIN: D; TRIACYLGLYCEROL	HYDROLASE; CHAIN: E;	TRIACYLGLYCEROL HYDROLASE; CHAIN: D; TRIACYLGLYCEROL HYDROLASE; CHAIN: E;	EPOXIDE HYDROLASE; CHAIN: A, B;	PROLYL AMINOPEPTIDASE; CHAIN: A;	TRIACYL-GLYCERÖL- HYDROLASE; CHAIN: D, E;
SEQFOL D score										80.11	
PMF	1.00	00'1	1.00	0.07	0.27	0.81		0.28	1.00		0.11
Verify	0.56	0.58	69:0	0.13	0.76	0.38		0.37	0.46		0.10
Psi Blast	1.2e-54	8e-43	3e-56	1.5e-06	4.5e-05	6e-25		4.8e-09	1.5e-45	6.4e-29	4.8e-10
END AA	356	356	958	226	215	238		212	358	360	215
STAR T AA	70	79	69	98	58	92		16	74	19	26
CHAI N ID	٧	В	8	A	Ą	۵		Q	4	<	Д
PDB ID	lek1	leki	1ek1	lhlg	1qe3	1qge		agpl	lqo7	lqtr	4lip
SEQ OS ES	1710	1710	1710	1710	1710	1710		1710	1710	1710	1710

PDB annotation	ANALOGUE, ENANTIOSELECTIVITY			METAL BINDING PROTEIN RING FINGER PROTEIN MATI; RING FINGER (C3HC4)	DINA-BINDIG PROTEIN V(DJ) RECOMBINATION ACTIVATING PROTEIN 1: RAGI, V(DJ) RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINGUELER CLUSTER, ZINC FINGER, DAA-BINDING PROTEIN	DAA-BINDING PROTEIN V(D)J RECOMBINATION ACTIVATING PROCTEIN I: RAGI, V(D)J RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINICILEAR CLUSTER, ZINC FINGER, DNA-BINDING PROTEIN	TOXIN BINDING PROTEIN TWO DOMAINS: BETA PROPELLER AND ALPHA/BETA FOLD	TRANSCRIPTION INHIBITOR BETA- PROPELLER
Coumpound		VIRUS EQUINE HERPES VIRUS- 1 (C3HC4, OR RING DOMAIN) 1 CHC 3 (NMR, 1 STRUCTURE) 1 CHC 4	VIRUS EQUINE HERPES VIRUS- 1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	CDK-ACTIVATING KINASE ASSEMBLY FACTOR MATI; CHAIN: A;	RAGI; CHAIN: NULL;	RAGI; CHAIN: NULL;	TOLB PROTEIN; CHAIN: A;	TRANSCRIPTIONAL REPRESSOR TUP1; CHAIN: A, B, C;
SEQFOL D score								
PMF		0.84	0.71	0.00	0.74	0.64	0.12	0.88
Verify score		-0.31	-0.18	-0.64	-0.02	-0.00	0.16	0.52
Psi Blast		6e-17	3.2e-14	4.5e-14	3e-11	1.3e-07	0.009	1.4e-28
END		328	332	321	328	331	297	307
STAR		275	278	276	272	280	194	171
CHAI N ID				Ą			4	A
PDB ID		Ichc	1chc	1g25	PEI I	Irmd	lcrz	lerj
SEQ NO D		1711	1711	11171	1711	1711	1712	1712

PDB annotation	TRANSCRIPTION INHIBITOR BETA- PROPELLER	COMPLEX (GTP. BINDMOOFTRANSDUCER) BETA1, TRANSDICAN BETA SUBUNT; GAMMAI, TRANSDUCIN GAMMA SUBUNT; COMPLEX (GTP. BINDMOOTRANSDUCER), G ROTER HETBERT BETANSDUCER, G ROTER HETBERT STRANSDUCER, G ROTER HETBERT STRANSDUCER, G	COMPLEX (GTP. BIDDMOTRANSDUCER) BETA1, TRANSDUCNE BETA SUBUNT; GAMMA, TRANSDUCIN GAMMA SUBUNT; COMPLEX (GTP. BIDDMOTRANSDUCER), GROTEN ROTEN, HETBOTTANER2 SIGNAL TRANSDUCTON	COMPLEX (GTP. BRUDINGTRANSDUCER) BETA1, RANSDUCIN BETA SUBURIT, GAMMAI, TRANSDUCIN GAMMA SUBURIT, COMPLEX (GTP. BRUDINGTRANSDUCER), G REVOTEN, HETEROTRIMER 2 SIGNAL TRANSDUCTION	STRUCTURAL GENOMICS HYPOTHETICAL PROTEIN, METHANOCOCCUS JANNASCHII	TRANSFERASE (METHYLTRANSFERASE) COMT; TRANSFERASE,
Coumpound	TRANSCRIPTIONAL REPRESSOR TUPI; CHAIN: A, B, C;	GT-ALPHAGG-ALPBA CHMERA, CHAIN: A; GT- BETA, CHAIN: B; GT-GAMMA; CHAIN: G;	GT-ALPHA/GI-ALPHA CHMERA, CHAIN: A; GT- BETA; CHAIN: B; GT-GAMMA; CHAIN: G;	GT-ALPHAGIANDHA CHIMBEN, CHAIN: A; GT. BETA, CHAIN: B; GT-GAMMA; CHAIN: G.	MJ0882; CHAIN: A;	CATECHOL O- METHYLTRANSFERASE; CHAIN; NULL;
SEQFOL D score			63.92			
PMF	96.0	1.00		1.00	0.43	0:30
Verify	0.33	0.43		0.54	-0.10	-0.07
Psi Blast	1.3e-44	6.4e-39	1.6e-48	1.6e-48	6.4e-10	7.50-11
END	289	290	307	305	446	455
STAR T AA	37	14	-	28	338	334
CHAI N ID	¥	m	m	m	¥	
PDB	lerj	Igot	Igot	lgot	1dus	lvid
SEQ No is	1712	1712	1712	1712	1713	1713

PDB annotation	METHYLTRANSFERASE, NEUROTRANSMITTER DEGRADATION			HYPERTHERMOSTABLE PROTEIN		HELICASE, 2 HYPERTHERMOSTABLE PROTEIN	Ī	BIFUNCTIONAL, PROTEASE- HELICASE	-	-	_	BC GENE REGULATION APO PROTEIN HAIN: A:	BC GENE REGULATION APO PROTEIN	ION TRANSLATION YEAST INITIATION		INITIATION FACTOR 4A, DEAD-BOX PROTEIN	Ė	INITIATION FACTOR 44; IF4A, HELICASE, DEAD-BOX PROTEIN		INITIATION FACTOR 4A; IF4A, HELICASE DEAD BOX PROTEIN	
Coumpound			DNA NUCLEOTIDE EXCISION REPAIR ENZYME UVRB; CHAIN: A;		DNA NUCLEOTIDE EXCISION REPAIR ENZYME UVRB;	CHAIN: A;	PROTEASE/HELICASE NS3;	CHAIN: A, B;	EXCINUCLEASE ABC SUBUNIT B: CHAIN: A:	EXCINICLEASE ABC SUBUNIT	B; CHAIN: A;	EXCINUCLEASE UVRABC COMPONENT UVRB: CHAIN: A:	EXCINICLEASE UVRABC	BUKARYOTIC INITIATION	FACTOR 4A; CHAIN: A;		YEAST INITIATION FACTOR	4A; CHAIN: A, B;	YEAST INITIATION FACTOR	4A; CHAIN: A, B;	
F SEQFOL c D score		_									_		_								-
PMF			0.53		96.0		0.77		0.62	98.0	_	0.99	0.43	0.18			0.35		-0.06		
Verify score			0.14		0.50		0.42		60.0	-0.11		0.35	0.20	0.07			0.02		0.04		
Psi Blast			3.2e-13		4.5e-I6		90000		3.2e-13	1.5e-16		3e-20	3.2e-18	1.1e-39			1.6e-25		0		
END			497		494		170		497	513		525	208	208			169		208		
STAR			345		371		20		3/15	370		346	354	338			2		119		
CHAI N ID			V		4		Ą		¥	A		٧	A	¥			4		æ		
PDB DD			1040		1040		Icul		1d2m	1d2m		149x	1d9x	1fuk			1fuu		1fuu		,
SEQ No:			1719		1719		1719		1719	1719		1719	1719	1719			6141		1719		

PDB annotation	INITIATION FACTOR 4A; IF4A, HELICASE, DEAD-BOX PROTEIN	HELICASE HELICASE, RNA, HEPATITIS, HCV, ATPASE, NTPASE	GENE REGULATION EIF44; TRANSLATION INITIATION, SACCHAROMYCES CEREVISIAE, DEAD BOX 2 PROTEIN FAMITY	HYDROLASE/DNA ATP-DEPENDENT HELICASE PCRA; ATP-DEPENDENT HELICASE PCRA; HELICASE PCRA, HYDROLASE, DNA, PRODUCT COMPLEX		INTEGRIN INTEGRIN, CELL ADHESION, GLYCOPROTEIN	INTEGRIN INTEGRIN, CELL ADHESION, GLYCOPROTEIN	COLLAGEN-BINDING COLLAGEN- BINDING, HEMOSTASIS, DINUCLEOTIDE BINDING FOLD	WILLEBRAND WILLEBRAND, BLOOD COAGULATION, PLATELET, GLYCOPROTEIN	WILLEBRAND WILLEBRAND, BLOOD COAGULATION, PLATELET, GLYCOPROTEIN	CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III	CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN
Coumpound	4A; CHAIN: A, B;	HCV HELICASE; CHAIN: A, B;	TRANSLATION INITIATION FACTOR 4A; CHAIN: A;	HELICASE PCRA; CHAIN: A, F; HELICASE PCRA; CHAIN: B, G; DNA (5-0° TP=TP=TP=T)-3'); CHAIN: C, D; DNA (5-10° 40P*C)-3'); 3'; CHAIN: H: DNA (5-	D(*AP*CP*TP*GP*C)-3); CHAIN: I;	INTEGRIN ALPHA 2 BETA; CHAIN: A. B:	INTEGRIN ALPHA 2 BETA; CHAIN: A, B;	VON WILLEBRAND FACTOR; CHAIN: A, B;	AI DOMAIN OF VON WILLEBRAND FACTOR; CHAIN: NUIT:	AI DOMAIN OF VON WILLEBRAND FACTOR; CHAIN: NUIL:	TITIN; CHAIN; NULL;	TITIN; CHAIN: NULL;
SEQFOL D score							75.90	89.44	65.12			
PMF		0.22	0.39	0.33		1.00				0.99	-0.01	0.41
Verify		0.29	0.10	0.22		0.62				0.79	0.22	0.65
Psi Blast		0.0014	3.2e-23	0.0006		1.le-21	1.1e-21	4.8e-17	I.6e-26	1.6e-26	3.2e-11	9e-12
END		170	169	82		170	220	213	221	220	302	427
STAR T AA		13	64	2		28	28	31	23	30	211	329
CHAI		¥	<	٧		4	∢	Ą				
PDB ID		Thei	Ide	2pjr		Iaox	Iaox	latz	lauq	lauq	1bpv	Ibpv
SEQ ID NO:		1719	1719	1719		1721	1721	1721	1721	1721	1721	1721

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PDB annotation	TYPE III	CONNECTIN A71, CONNECTIN; TITIN, CONNECTIN, FIBRONECTIN TYPE III	SIGNALING PROTEIN CYTOKINE RECEPTOR, GLYCOPROTEIN 130, GP130, INTERLEUKINE 6.2 RECEPTOR BETA SUBUNIT, SIGNALING PROTEIN											STRICTIMAL PROTEIN L DOMANIN	METAL BINDING, COLLAGEN, ADHESION	STRUCTURAL PROTEIN I-DOMAIN, METAL BINDING, COLLAGEN,	Apriliation
Соптроип		TITIN; CHAIN: NULL;	GP130; CHAIN: A, B;	NEURAL ADHESION MOLECULE DROSOPHILA NEUROGLIAN	(CHYMOTRYPTIC FRAGMENT CONTAINING THE LCFB 3 TWO	AMINO PROXIMAL	REPEATS ICFB 4 (RESIDUES	NET BAL ADDISTON	MOLECULE DROSOPHILA NEUROGLIAN	(CHYMOTR YPTIC FRAGMENT	CONTAINING THE ICFB 3 TWO	FIBRONECTIN TYPE III	REPEATS ICFB 4 (RESIDUES	INTEGRIN AI PHA-1: CHAIN: 4	В;	INTEGRIN ALPHA-1; CHAIN: A, B;	CELL ADHESION PROTEIN
SEQFOL D score				52.60													
PMF		60:0	0.48					0.07	2					1 00		1.00	0.72
Verify		0.47	0.45					900	3					0.46	2	96.0	0.49
Psi Blast		3.2e-13	3.2e-12	1.4e-11				1 40-11						9.66-21		6e-38	1.1e-13
END		418	419	427				412						170		209	415
STAR		342	337	208				200	}					33		34	338
CHAI N ID			¥											V	:	¥	
PDB ID		16pv	1bqu	1cfb				100	2					1ck4		1ck4	1fna
SEQ ID NO:		1721	1721	1721				1721						1721		1721	1721

PDB annotation		CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX IFNF 18	CELL ADHESION PROTEIN RGD, EXTRACEL ULAR MATRIX IFNE 18	CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX IPNF 18	HEPARIN AND INTEGRIN BINDING HEPARIN AND INTEGRIN BINDING	HEPARIN AND INTEGRIN BINDING HEPARIN AND INTEGRIN BINDING	HEPARIN AND INTEGRIN BINDING HEPARIN AND INTEGRIN BINDING	IMMUNE SYSTEM VON	GLYCOPROTEIN IBA (A:ALPHA)	BINDING, 2 COMPLEX	(WILLEBRAND/IMMUNOGLOBULIN	VON WILLEBRAND DISEASE	CELL ADHESION PROTEIN A-	DOMAIN INTEGRIN, CELL	ADHESION PROTEIN, GLYCOPROTEIN, EXTRACELLULAR	2 MATRIX, CYTOSKELETON	CELL ADHESION PROTEIN A-	DOMAIN INTEGRIN, CELL	ADHESION PROTEIN,	2 MATRIX, CYTOSKEL ETON	CELL ADHESION LFA-1, ALPHA- L\BETA-2 INTEGRIN, A-DOMAIN;
Coumpound	FIBRONECTIN CELL- ADHESION MODULE TYPE III- 10 IFNA 3	FIBRONECTIN; 1FNF 6 CHAIN: NULL; 1FNF 7	FIBRONECTIN; 1FNF 6 CHAIN:	FIBRONECTIN; 1FNF 6 CHAIN: NULL: 1FNF 7	FIBRONECTIN; CHAIN: A;	FIBRONECTIN; CHAIN: A;	FIBRONECTIN; CHAIN: A;	IMMUNOGLOBULIN NMC-4	IMMUNOGLOBULIN NMC-4	IGG1; CHAIN: H; VON	WILLEBRAND FACTOR; CHAIN: A:	CITATION 13,	INTEGRIN; CHAIN: NULL;				INTEGRIN; CHAIN: NULL;				CD11A; ILFA 5 CHAIN: A, B; ILFA 6
SEQFOL D score				91.50		73.33							91.05								78.17
PMF		0.13	-0.06		-0.09		0.49	1.00									1.00				
Verify score	-	-0.05	-0.00		9.16		-0.04	0.97									0.65				
Psi Blast		1.4c-26	1.6e-31	1.6e-31	1.6e-24	1.1e-26	1.1e-26	1.6e-25					7.5e-37				7.5e-37				1.5e-36
END		444	415	425	421	421	445	217					208				206				213
STAR T AA		106	27	28	107	133	213	30					32				34				33
CHAI					۷.	V	V	4													٧
10 E		1fnf	Juj1	1finf	1fnh	1fmh	1fnh	1fns					1ido				lido				11fa
SEQ El Sign		1721	1721	1721	1721	1721	1721	1721					1721				1721				1721

PDB annotation	1LFA 8	CELL ADHESION LFA-1, ALPHA- L'ABTA-2 INTEGRIN, A-DOMAIN; 1LFA 8	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCORROTEIN	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN	CELL ADHESION INTEGRIN, CELL ADHESION	CELL ADHESION INTEGRIN, CELL ADHESION	STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2 PROTEIN	STRUCTURAL PROTEIN TENASCIN, FURRONECTIN TYPE-II; HEPARIN, EXTRACELLULAR 2 MATRUX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN
Coumpound		CD11A; ILFA 5 CHAIN: A, B; ILFA 6	FIBRONECTIN; CHAIN: NULL;	FIBRONECTIN; CHAIN: NULL;	FIBRONECTIN; CHAIN: NULL;	ALPHAI BETAI INTEGRIN; CHAIN: A; ALPHAI BETAI INTEGRIN; CHAIN: B;	ALPHAI BETAI INTEGRIN; CHAIN: A; ALPHAI BETAI INTEGRIN; CHAIN: B;	INTEGRIN BETA 4 SUBUNIT; CHAIN: A, B;	TENASCIN; CHAIN: A, B;
SEQFOL D score			75.51						
PMF		1.00		0.58	0.37	1.00	1.00	-0.07	0.72
Verify		89.0		80.0	0.42	0.55	66.0	0.05	0.04
Psi Blast		1.56-36	6.4e-24	6.4e-24	8e-17	8e-21	7.5e-28	1.6e-18	1.6e-22
END AA		209	425	415	445	170	209	419	421
STAR		34	211	215	342	30	34	214	214
CHAI N ID		∢				<	<	Ą	<
PDB GI		11fa	lmfin	1mfh	mfm m	lqc5	19c5	1qg3	1qr4
SEQ NO.		1721	1721	1721	1721	1721	1721	1721	1721

PDB annotation	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-III, HEPARIN, EXTRACELJULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-III, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN				PROTEIN BINDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2 BINDING	PROTEIN BINDING ED-B, FIBRONECTIN, TYPEIII DOMAIN, ANGIOGENESIS, PROTEIN 2	COAGULATION FACTOR	٠
Соитроип	TENASCIN; CHAIN: A, B;	TENASCIN; CHAIN: A, B;	CELL ADHESION PROTEIN TENASCIN (THIRD FIBRONECTIN TYPE III REPEAT) ITEN 3	CELL ADHESION PROTEIN TENASCIN (THIRD FIBRONECTIN TYPE III REPEAT) ITEN 3	GLYCOPROTEIN FIBRONECTIN (TENTH TYPE III MODULE) (NMR, 36 STRUCTURES) ITTF 3	FIBRONECITN; CHAIN: A;	FIBRONECTIN; CHAIN: A;	HUMAN TISSUE FACTOR; 2HFT 4 CHAIN: NULL; 2HFT 5	HORMONE/RECEPTOR HUMAN GROW/TH HORMONE COMPLEXED WITH ITS
SEQFOL D score	77.31								
PMF		0.34	0.99	18:0	0.70	0.84	0.86	-0.17	-0.19
Verify score		0.55	90:0	0.92	0.27	0.55	0.71	80.0	80.0
Psi Blast	1.6e-22	1.4e-13	3e-12	1.2e-13	3.2e-14	1.3e-06	3.2e-11	1.16-12	1.5e-16
END	421	445	301	421	415	281	421	416	422
STAR	214	337	210	335	337	215	337	215	215
CHAI N ID	¥	¥				٧	∢		æ
PDB ID	1qr4	lqr4	Iten .	Iten	Jiij	2fnb	2fib	2hft	3hhr
SEQ NO:	1721	1721	1721	1721	1721	1721	1721	1721	1721

PDB annotation		MANAGEMENT AND	TRANSLATION EUKARYOTIC INITIATION FACTOR 44; IF44, HELICASE, DEAD-BOX PROTEIN	_ ` `	CALCIUM/CALMODULIN																							COMPLEX (KINASE/INHIBITOR)
Coumpound	RECEPTOR 3HHR 3 (EXTRACELLULAR DOMAIN) 3HHR 4		YEAST INITIATION FACTOR 4A; CHAIN: A, B;	CALCIUM/CALMODULIN- DEPENDENT PROTEIN KINASE;	CHAIN: NULL;	TRANSFERASE(PHOSPHOTRA	NSFERASE) \$C-/AMP\$-	DEPENDENT PROTEIN KINASE	(E.C.2.7.I.37) (\$C/APK\$) 1APM 3	(CATALYTIC SUBUNIT) ALPHA	ISOENZYME MUTANT WITH	SER 139 1APM 4 REPLACED BY	ALA (/S139AS) COMPLEX WITH	THE PEPTIDE 1APM 5	INHIBITOR PKI(5-24) AND THE	DETERGENT MEGA-8 1APM 6	TRANSFERASE(PHOSPHOTRA	NSFERASE) \$C-/AMP\$-	DEPENDENT PROTEIN KINASE	(E.C.2.7.1.37) (\$C/APK\$) 1APM 3	(CATALYTIC SUBUNIT) ALPHA	ISOENZYME MUTANT WITH	SER 139 1APM 4 REPLACED BY	ALA (/S139AS) COMPLEX WITH	THE PEPTIDE 1APM 5	INHIBITOR PKI(5-24) AND THE	DETERGENT MEGA-8 TAPM 6	CYCLIN-DEPENDENT KINASE
SEQFOL D score																	59.46											25.32
PMF			0.58	0.27		0.88																						
Verify			0.19	-0.31		-0.22																						
Psi Blast			4.5e-06	4.8e-39		3.2e-47											3.2c-47											8c-24
END			236	355		356											413										1	333
STAR T AA			146	147		143											11											5
CHAI			В			ш											ш											V
EDB EDB			1fun	1a06		lapm			_	-							lapm											1018
SEQ NO:			1723	1724		1724											1724										_	1/74

PDB annotation	CURG, PISINKAD, CYCLIN DEPENDENT KINAGE, CYCLIN DEPENDENT KINAGE, INHIBTORY 2 PROTEN, CDK, INK4, CELL CYCLE, COMPLEX KINASEINHBITOR) HEADER HELJX				·	TRANSFERASE KINASE DOMAIN, AUTOINHBITORY FRAGMENT, HOMODIMER	SERINEJTHREONING-PROTEIN KINASE CSBP. RK, P38, PROTEIN SERTHR-KINASE, SERNNEJTHREONING-PROTEIN KINASE
Coumpound	6; CHAIN: A, C; CYCLIN- DEPENDENT KINASE INHIBITOR; CHAIN: B, D;	PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT ICMK 3 (E.C.2.7.1.37) ICMK 4	PHOSPHOTRANSFERASE CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT 1CMK 3 (E.C.2.7.1.37) 1CMK 4	TRANSFERASE(PHOSPHOTRA NSFERASE) CAMP. DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) ICTP 3 (CATAL 7TIC SUBUNIT) ICTP 4	TRANSFERASE(PHOSPHOTRA NSFERASE) CAMP. DEPENDENT PROTEIN KINASE (E.C.2.7.1.37) (CAPK) 1CTP 3 (CATALYTIC SUBUNIT) 1CTP 4	SERINETTHREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: A, B; SERINE/THREONINE- PROTEIN KINASE PAK-ALPHA; CHAIN: C, D;	P38 MAP KINASE; CHAIN: NULL;
SEQFOL D score			59.27		58.35		56.49
PMF		0.70		0.77		0.54	
Verify score		-0.22		-0.14		0.07	
Psi Blast		1.6e-48	1.6e-48	1.6e-48	1.6e-48	4.8e-36	1.fe-18
END		356	413	356	399	361	401
STAR T AA		143	69	143	11	147	77
CHAI		m	щ	ш	ш	ن	
PDB.		lcmk	lcmk	lctp	letp	113m	lian
SEQ No ib		1724	1724	1724	1724	1724	1724

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PDB annotation	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE:	TRANSFERASE, MAP KINASE, SERINETHREONINE-PROTEIN KINASE, 2 P.38	KINASE RABBIT MUSCLE	PHOSPHORYLASE KINASE;	GLYCOGEN METABOLISM, TRANSFERASE,	SERINE/THREONINE-PROTEIN, 2	KINASE, ATP-BINDING,	CALMODULIN-BINDING	TRANSFERASE MAP KINASE,	SEKINE/THREONINE PROTEIN KINASE, TRANSFERASE	TRANSFERASE MAP KINASE.	SERINE/THREONINE PROTEIN	KINASE, TRANSFERASE	SERINE KINASE SERINE KINASE,	HILLY, MOSCLE, AUTOINFIBITION	AMINE/CARBOXYLATE LIGASE	AMINE/CARBOXYLATE LIGASE		COMPLEX (NUCLEAR BROTTEIN BANA) COMPLEY	ONICE BAR PROTEIN/BNA) DNA	SNRNP.RIBONUCLEOPROTEIN	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING
Coumpound	TWITCHIN; CHAIN: NULL;	TWITCHIN; CHAIN: A, B;	MAP KINASE P38; CHAIN: NITL:		PHOSPHORYLASE KINASE;	CHAIN: NULL;					ERK2; CHAIN: NULL;		ERK2: CHAIN: NULL:	Î		TITIN; CHAIN: A, B;		GLUTATHIONE SYNTHETASE;	CHAIN: A;		D. 112 A.: CHAIN! A C. 112 D.:	CHAIN: B.D.		SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'-
SEQFOL D score			60.82										58.82											
PMF	0.11	0.55			0.81						0.13					0.54		0.52			0.32			0.95
Verify	-0.27	-0.31			0.03						0.10					-0.27		-0.23		9,0	0+			0.26
Psi Blast	1.1e-33	6.4e-34	1.6e-24		3.2e-43						1.1e-24		1.1e-24			3.2e-27		0.0088			/0-90/			9e-05
END	356	356	403		356						414		392			362		99	ĺ		666			919
STAR T AA	148	150	42		127						162		83			150		3		,00	000			542
CHAI N ID		Α								I						∢		¥	Ī		۵.			V
PDB ID	Ikoa	1kob	1p38		1phk					1	Ipme		Ipme			¥		2hgs	Ì		116211			1b7f
SEQ NO:	1724	1724	1724		1724					100	1724		1724			1724		1726		1700	07/1			1728

SRO PAB CHA STAR RAD FAB Blast Verify PAMF Storr Decret Decret			_			_				_						_					_	_	_		_		_		_	
Pub CiAA STAR RND Fi Blank Verify Purp SEQPOLO	PDB annotation	REGULATION, RNP DOMAIN, RNA COMPLEX	RNA-BINDING PROTEIN/RNA TRA	PRE-MRNA; SPLICING PECHI ATTON BND DOMAIN PNA	COMPLEX	STRUCTURAL PROTEIN TWO	REPEATS OF SPECTRIN, ALPHA	HELICAL LINKER REGION, 22	TANDEM 3-HELIX COILED-COILS,	SIRUCIURAL PROIEIN	BINDING PROTEIN 1 PARD 1: PPM	PROTEIN, RNA COMPLEX GENE	REGIL ATTON/RNA			GENE REGULATION/RNA POLY(A)	BINDING PROTEIN 1, PABP 1; RRM,	PROTEIN-RNA COMPLEX, GENE	REGULATION/RNA		CENT DE CITATION (BALLANDE POLITICALITY)	BINDING PROTEIN 1 DARD 1: PDM	PROTEIN-RNA COMPLEX GENE	REGULATION/RNA			RNA BINDING PROTEIN/RNA	NESTED DOUBLE PSEUDOKNOT	RNA STRUCTURE	RNA BINDING PROTEIN RNA- BINDING DOMAIN
PB CIAA STAR EAD P4 Blast Verify Fuffer	Coumpound	R(P*GP*UP*UP*UP*UP*UP*UP*UP* UP*UP*UP*UP*UP*U)- CHAIN: P, O;	SXL-LETHAL PROTEIN; CHAIN:	A, B; RNA (5'- B (0*/30*) D* (10*)	UP*UP*UP*UP*U)- CHAIN: P, Q;	ALPHA SPECTRIN; CHAIN: A,	B,C			Contract of the contract of th	PROTTEIN 1: CHAIN: A B C D	E F G H- RNA (51.	R(*AP*AP*AP*AP*AP*AP*	AP*AP*AP*A); CHAIN: M. N.	O, P, Q, R, S, T;	POLYDENYLATE BINDING	PROTEIN 1; CHAIN: A, B, C, D,	E, F, G, H; RNA (5'-	R(*AP*AP*AP*AP*AP*AP*	AP*AP*AP*A)-3'); CHAIN: M, N,	O, P, Q, R, S, T;	PROTEIN I CHAIN A B C D	E. F. G. H: RNA (51-	R(*AP*AP*AP*AP*AP*AP*	AP*AP*AP*A)-3'); CHAIN: M, N,	O, P, Q, R, S, T;	UIA PROTEIN; CHAIN: A; HDV	RIBOZYME SELF-CLEAVED;	CHAIN: B;	HU ANTIGEN C; CHAIN: A;
PDB CHAI STAR END F9 Blast Verify	SEQFOL D score																													
PDB CHAI STAR END F4 Blast PB Bl	PMF		0.43			0.10				90.	97.					0.57					0.43	Ç.					0.53			0.53
PB CHAI STAR END ID NID TAA AA AA ID A 8899 958 10m A 720 835 10m A 544 612 10m A 889 956 10m A 889 956 10m A 889 956 10m 10m A 840 614 10m 614 10m A 840 614 10m 614 10m A 840 614 10m A 840 614 10m A 840	Verify		80.0			-0.04				9.0	2					0.47					0 54	<u> </u>					-0.15			0.64
PDB CHAI STAR	Psi Blast		3e-07			0.003				00.00	1.35-03					7.5e-07					7 54 07	70-00-7					6e-05			1.5e-05
PDB CHAI	END		856			835					710					926					050	2					614			614
100 100	STAR T AA		688			720				24.4	ŧ					688		_			552	è					540	_		540
	CHAI N ID		٧			A				-	<		_			¥					£:	,					V			< 1
850, No. n	PDB UD		1 b 7f			Icun					levi					levj					loui.	5					1cx0			1d8z
	SEQ NO:		1728			1728				1700	07/1					1728					1738	3					1728			1728

PDB annotation	RNA BINDING PROTEIN RNA- BINDING DOMAIN	ENDOCYTOSIS/EXOCYTOSIS NSECI; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT	KIBONUCLEOPROTEIN UTA117; RIBONUCLEOPROTEIN, RNP DOMAIN, SPLICEOSOME	STRUCTURAL PROTEIN PROTEIN C23; RNP, RBD, RRM, RNA BINDING DOMAIN, NUCLEOLUS	NUCLEAR PROTEIN HETROGORISOUS NUCLEAR RIBOAUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRNA, RNP, RNA BINDING, 2 RIBOAUCLEOPROTEIN	RNA BINDING PROTEIN RNA- BINDING DOMAIN		KIBONUCLEOPROTEIN PTB, PTB- C198, HETEROGENBOUS NUCLEAR POLYPYRMIDINE TRACT BINDING PROTEIN, RNP, RNA, SPICING, 2 TRANSLATION
	RNA	NSEC SOM SOM SOM SOM SOM SOM SOM SOM SOM SOM	M M M	STR S. S. S.	READ NOT	BINI		RIBC C198 POLY PROT
Coumpound	HU ANTIGEN C; CHAIN: A;	SYNTAXIN BINDING PROTEIN 1; CEAIN: A; SYNTAXIN 1A; CHAIN: B;	UI SMALL NUCLEAR RIBONUCLEOPROTEIN A; CHAIN: NULL;	NUCLEOLIN RBD1; CHAIN: A;	HNRNP A1; CHAIN: NULL;	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN DO; CHAIN: A;	RIBONUCLEOPROTEIN PROME IN SWALL NUCLEAR RIBONUCLEOPROTEIN (SNRNP U) INRC 3 (FATERAINAL PRAGMENT, RESIDUES 1- 95) MUTANT WITH GLN 85 INRC 4 REPLACED BY CYS (QSC) INRC 5	POLYPYRIMIDINE TRACF. BINDING PROTEIN; CHAIN: A;
SEQFOL D score								
PMF	0.80	0.37	89.0	0.21	66.0	0.71	66:0	0.22
Verify score	0.48	-0.23	0.65	0.48	0.42	0.32	0.13	-0.14
Psi Blast	3e-05	3e-06	1.5e-05	6e-07	1.5e-05	6e-07	10-08	7.5e-05
END	865	835	614	947	612	614	946	614
STAR T AA	542	402	540	887	541	995	988	493
CHAI	V	В		V		V	д	Ą
FDB EDB	1d9a	ldnI	1fbt	1£7	Tha I	1hd1	linc	lqm9
SEQ NO:	1728	1728	1728	1728	1728	1728	1728	1728

PDB annotation	RIBONUCLEOPROTEIN PTB, PTB- C198, HETEROGENEOUS NUCLEAR POLYPYRIMIDINE TRACT BINDING PROTEIN, RNP, RNA, SPICING, 2 TRANSLATION		COMPLEX (RIBONUCLEOPROTEINRNA)	RNA BINDING PROTEIN RNA- BINDING DOMAIN	RNA-BINDING DOMAIN RNA- BINDING DOMAIN, ALTERNATIVE SPLICING	NUCLEAR PROTEIN UI SNRNP A PROTEIN; RNA BINDING DOMAIN, NUCLEAR PROTEIN	NUCLEAR PROTEIN UI SNRNP A PROTEIN; RNA BINDING DOMAIN, NUCLEAR PROTEIN	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP AI, UPI; COMPLEX (RIBONUCLEOPROTEIN/DNA).
Соитронид	POLYPYRIMIDINE TRACT- BINDING PROTEIN; CHAIN: A;	RNA-BINDING PROTEIN SEX- LETHAL PROTEIN (C. TRAMINUS, OR SECOND RNA- BINDING DOMANI 1 SXL. 3 (RBD-2), RESIDDES 199-294 PLUS N-TERMINAL MET) 1 SXL 4 (NMR, 17 STRICCTURES) 1 SXL.	UIA SPLICEOSOMAL PROTEIN; IURN 5 CHAIN: A, B, C, IURN 6 RNA 2 IMER HARPIN (5*- (AP*AP*UP*CP*CP*AP*UP*UP* IURN II CHAIN: P, Q, R IURN 13	MUSASHII; CHAIN: A;	SEX-LETHAL PROTEIN; CHAIN: NULL;	UI SMALL NUCLEAR RIBONUCLEOPROTEIN A; CHAIN: NULL;	UI SMALL NUCLEAR RIBONUCLEOPROTEIN A; CHAIN: NULL;	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED
SEQFOL D score								
PMF	0.10	0.82	0.40	0.03	0.75	0.39	0.43	0.75
Verify	0.10	0.51	-0.03	-0.03	0.18	0.42	0.05	0.51
Psi Blast	1.5e-07	0.0001	10000	1e-06	4.5e-06	3e-05	20 - 99	7.5e-07
END	947	610	619	614	614	919	946	612
STAR T AA	828	240	540	095	542	542	887	525
CHAI	∀		A	V				<
FDB ID	lqm9	ixi ixi	lum	2mss	2sxl	2ula	2ula	2up1
SEQ ID NO:	1728	1728	1728	1728	1728	1728	1728	1728

			2.6	8.8	Т. Т	1
PDB annotation	HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN AI	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRIP A.I. UPI; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETTROGENBOUS NUCLEAR 2 RIBONUCI ROPROTEIN A I	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLCKNO INTIBITOR, TRANSIATIONAL INHBITOR, SEX 3 DETERMINATION, CHROMOSOME DOSAGE COMPENSATION	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHBITOR, TRANSLATIONAL HIBIETTOR, SEX 3 DETTERMINATION, X CHROMOSOME DOSAGE COMPENSATION	PLASMA PROTBIN PLASMA PROTBIN, METAL-BINDING, LIPID- BINDING	
Coumpound	TELOMETRIC DNA; CHAIN: B;	HETEROGENEOUS NÜCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A: 12:NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	SEX-LETHAL; CHAIN: A, B, C;	SEX-LETHAL; CHAIN: A, B, C;	SERUM ALBUMIN; CHAIN: A;	DNA-BINDING PROTEIN ANTENNA-BEDIA, PROTEIN (HOMEODOMAIN) MUTANT WITH CYS 39 I AHD 3 REFLACED BY SER (C39S) COMPLEX WITH POXA (NAM) I AHD 4 16 STRUCTURES) I AHD
SEQFOL D score						
PMF		0.95	1.00	0.48	0.17	0.18
Verify score		0.32	0.58	0.38	-0.27	-0.46
Psi Blast		7.5e-07	10-05	3e-07	0.0015	1.16-28
END AA		947	612	958	336	347
STAR T AA		888	542	888	199	267
CHAI N ID		¥	<	۷	4	e.
PDB		2up1	3sxl	3sxl	le7f	lahd
SEQ ID NO:		1728	1728	1728	1730	1733

u.		OMAIN, INDING	PROTEIN; DOMAIN, IFICITY	IG MDING BOX, JLATION	IG MDING BOX, JLATION				
PDB annotation		PROTEIN/DNA HOMEODOMAIN DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA	TRANSCRIPTION/DNA ULTRABITHORAX, FBX PROTEIN; DNA BINDING, HOMEODOMAIN, HOMEOTIC PROTEINS, DEVELOPMENT, 2 SPECIFICITY	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION				
Coumpound	2	HOMEOBOX PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E;	ULTRABITHORAX HOMEOTIC PROTEIN IV, CHAIN: A; HOMEOBOX PROTEIN EXTRADENTICLE, CHAIN: B; DDNA (5° CHAIN: C; DNA (5° CHAIN: D;	PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	TRANSCRIPTION REGULATION TRANSCRIPTION FACTOR LFB1 (HOMEODOMAIN) 1LFB 3	GENE REGULATING PROTEIN REPRESSOR PROTEIN FROM BACTERIOPHAGE 434 (DNA- BINDING 1PRA 3 DOMAIN, RESIDUES 1-69) (NMR, 20 STRUCTURES) 1PRA 4	GENE REGULATING PROTEIN REPRESSOR (AMINO- TERMINAL DOMAIN) (R.I-69) 1R69 4	DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN (HOMEODOMAIN) MUTANT
SEQFOL D score									
PMF		0.07	0.46	0.92	1.00	0.99	0.51	0.78	61.0
Verify		-0.02	-0.12	-0.04	0.38	0.61	0.08	0.15	0.09
Psi Blast		6.4e-24	6.4e-24	3.2e-23	9.6e-22	6e-24	0.00015	0.0003	1.6e-26
END		343	340	341	339	336	205	205	347
STAR T AA		271	270	266	267	271	173	173	273
CHAI N ID		<	∢	٧	В				
PDB UI		1672	1681	191	101	11fb	lpra	lr69	Isan
SEQ ID NO:		1733	1733	1733	1733	1733	1733	1733	1733

PDB annotation		TRANSCRIPTION REGULATION GENE REGULATING PROTEIN, TRANSCRIPTION REGULATION		COMPLEX (DNA-BINDING PROTEIN/DNA) HD; HOMEODOMAIN, COMPLEX (DNA- BINDING PROTEIN/DNA)	·	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA	TRANSCRIPTION/DINA ULTRABITHORAX; PROTEIN; DINA BINDING, HOMEODOMAIN, HOMEOTIC PROTEINS DEVELOPMENT, 2 SPECIFICITY	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING
Coumpound	WITH CYS 39 ISAN 3 REPLACED BY SER AND RESIDUES 1-6 DELETED (C39S,DEL 1-6) ISAN 4 (NMR, 20 STRUCTURES) ISAN 5	PHAGE 434 CRO PROTEIN; CHAIN: NULL;	GENE REGULATING PROTEIN CRO PROTEIN 2CRO 4	ANTENNAPEDIA PROTEIN; CHAIN: A, B; DNA; CHAIN: C, D, E, F;		HOMEOBOX PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; DNA CHAIN: B;		PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F
SEQFOL D score								
PMF		0.17	0.29	0.04	0.18	0.07	0.28	0.92
Verify score		-0.16	-0.59	-0.27	-0.46	-0.02	-0.31	-0.04
Psi Blast		0.0003	0.0003	3.2e-26	1.6e-28	1.6e-24	8e-24	1.6e-23
END		205	205	341	347	343	340	341
STAR T AA		173	173	271	267	271	271	266
CHAI N ID				∢	p.	∢	<	4
ros O		lzug	2cro	9ant	lahd	1672	168i	191
S e S		1733	1733	1733	1734	1734	1734	1734

				_										
PDB annotation	PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION	COMPLEX (DNA-BINDING PROTEIN/DNA) DNA-BINDING PROTEIN, DNA, PAIRED BOX, TRANSCRIPTION 2 REGULATION										TRANSCRIPTION REGULATION GENE REGULATING PROTEIN, TRANSCRIPTION REGULATION		COMPLEX (DNA-BINDING PROTEIN/DNA) HD;
Coumpound		PAIRED PROTEIN; CHAIN: A, B, C; DNA; CHAIN: D, E, F	TRANSCRIPTION REGULATION TRANSCRIPTION FACTOR LFB1 (HOMEODOMAIN) 1LFB 3	GENE REGULATING PROTEIN REPRESSOR PROTEIN FROM	BACI EMOPHAGE 434 (DNA- BINDING 1PRA 3 DOMAIN, RESIDUES 1-69) (NMR, 20 STRICTI IDEN 1DR 4.4	GENE REGULATING PROTEIN REPRESSOR (AMINO- TERMINAL DOMAIN) (R1-69)	1R69 4	DNA-BINDING PROTEIN ANTENNAPEDIA PROTEIN HOMPODOMAIN MITTANT	WITH CYS 39 1SAN 3	REPLACED BY SER AND RESIDITES 1.6 DET FTED	(C39S,DEL 1-6) 1SAN 4 (NMR, 20 STRUCTURES) 1SAN 5	PHAGE 434 CRO PROTEIN; CHAIN: NULL;	GENE REGULATING PROTEIN CRO PROTEIN 2CRO 4	ANTENNAPEDIA PROTEN; CHAIN: A, B; DNA; CHAIN: C,
SEQFOL D score														
PMF		1.00	66:0	0.51		0.78		0.19				0.17	0.29	0.04
Verify		0.38	0.61	0.08		0.15		60:0				-0.16	-0.59	-0.27
Psi Blast		8e-22	6e-24	0.00015		0.0003		6.4e-26				0.0003	0.0003	8e-26
END		339	336	205		205		347				205	205	341
STAR T AA		267	27.1	173		173		273				173	173	27.1
CHAI N ID		В												۷ .
PDB ID		191	g][lpra		1169		Isan				lzug	2cro	9ant
SEQ No ed		1734	1734	1734		1734		1734				1734	1734	1734

CHAI STAR I			END	Psi Blast	Verify	PMF	SEQFOL D score	Coumpound Coumpound	PDB annotation HOMEOTOMATN COMPLEX (DNA.
								ii ii ii	HUMEUDOMAIN, COMPLEX (DNA- BINDING PROTEIN/DNA)
1 101 4,8			8.	4.8e-30	-0.11	90:0		TROPONIN C; CHAIN: NULL;	MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCIUM BINDING
23 170 1.4	170		1.4	1.4e-38			82.97	TROPONÍN C; CHAIN: NULL;	MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCIUM BINDING
25 169 1.4e	169		1.4e	1.4e-38	0.17	0.70		TROPONIN C; CHAIN: NULL;	MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCIUM BINDING
30 104 1.1e-29	104		1.1e	29			75.36	CALMODULIN; CHAIN: NULL;	CALCTÚM-BINDING PROTEIN CALMODULIN CERUM TRIC- DOMAIN, RESIDUES I - 75; CERUM- LOADED, CALCTÚM-BINDING PROTEIN
22 109 6.4e-23	601		6.46-	53			61.36	CARDIAC N-TROPONIN C; CHAIN: NULL;	CALCIUM-BINDING CYTNC; CALCIUM-BINDING, REGULATION, TROPONIN C, CARDIAC MUSCLE 2 CONTRACTION
101	101		3.2e-	20	80.0	-0.01		SERINE/THREONINE PHOSPHATASE 2B; CHAIN: A, B;	HYDROLASE CALCINEURIN; HYDROLASE, PHOSPHATASE, IMMUNOSUPPRESSION
A 26 106 3.2c-26	106		3.26	26			70.90	TROPONIN C; CHAIN: A, B;	MUSCLE CONTRACTION MUSCLE CONTRACTION, CALCIUM- ACTIVATED, TROPONIN, E-F HAND 2 CALCIUM-BINDING PROTEIN
20 109 8e-27	109		86-2	_			71.63	N-TROPONIN C; CHAIN: NULL;	CALCIUM-BINDING PROTEIN SINTING; CALCIUM-BINDING, REGULATION, TROPONIN C, SKELETAL MUSCLE, 2 CONTRACTION
B 33 170 4.8e-34	170	П	4.8e-	34			57.30	MYOSIN; CHAIN: A, B, C, D, E,	MUSCLE PROTEIN MDE; MUSCLE

PDB annotation	PROTEIN	CALCIUM BINDING CALCIUM BINDING																				The state of the s						CALCIUM-BINDING PROTEIN CALMODULIN APO TR2C-DOMAIN; ICMF 9	STRUCTURAL PROTEIN HELIX-
Coumpound	F, G, H;	CALCIUM-BINDING PROTEIN; CHAIN: NULL;	CALCIUM-BINDING PROTEIN	CALMODULIN COMPLEXED	MILE CALMODOLIN-BINDING	CAI MODITI IN DEPENDENT	PROTEIN KINASE II 1CDM 4	CALCIUM-BINDING PROTEIN	CALMODULIN COMPLEXED	WITH CALMODULIN-BINDING	DOMAIN OF 1CDM 3	CALMODULIN-DEPENDENT	PROTEIN KINASE II 1CDM 4	CALCIUM-BINDING PROTEIN	CALMODULIN COMPLEXED	WITH CALMODULIN-BINDING	DOMAIN OF 1CDM 3	CALMODULIN-DEPENDENT	PROTEIN KINASE II 1CDM 4	CALCIUM-BINDING PROTEIN	CALMODULIN (VERTEBRATE)	CALCILM-BINDING PROTEIN	CALMODULIN (VERTEBRATE)	1CLL 3	CALCIUM-BINDING PROTEIN	CALMODULIN (VERTEBRATE)	ICLL 3	CALMODULIN (VERTEBRATE); 1CMF 6 CHAIN: NULL; 1CMF 7	CARDIAC TROPONIN C;
SEQFOL D score		50.72						85.63	•																89.82			68.52	
PMF			0.82											0.92						0.40		0.81							0.28
Verify score			10.0											80.0						. 60.0		-0.02							00:00
Psi Blast		3.2e-11	8e-35					1.4e-47						1.4e-47						3.2e-35		9.6e-53	_		9.6e-53			7.5e-23	4.8e-29
END		103	102					158						169						102		169			1.70			104	101
STAR T AA		2					_	33						33						_		33			33			83	
CHAI N ID			K					٧						Ψ															Ą
PDB ID		1bu3	Icdm					lcdm			_			Icdm						7		Icli			IcI			Icmf	1drl
SEQ ID NO:		1738	1738					1738						1738		_				1738		1738			1738			1738	1738

PDB annotation	TURN-HELIX	STRUCTURAL PROTEIN HELIX- TURN-HELIX	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER						CALCIUM-REGULATED MUSCLE	CONTRACTION MUSCLE CONTRACTION, CALCIUM-	BINDING, TROPONIN, E-F HAND, 2	OPEN CONFORMATION	REGULATORY DOMAIN, CALCIUM-	CONTRACTION	CALCIUM-REGULATED MUSCLE	CONTRACTION MUSCLE	CONTRACTION, CALCIUM-	BINDING, IROPONIN, E-F HAND, 2 OPEN CONFORMATION	REGULATORY DOMAIN, CALCIUM-	REGULATED 3 MUSCLE	CONTRACTION	CALCIUM-REGULATED MUSCLE CONTRACTION MUSCLE
Coumpound	CHAIN: A;	CARDIAC TROPONIN C; CHAIN: A;	CALMODULIN; CHAIN: A;	CALMODULIN; CHAIN: A;	CALCIUM BINDING PARVALBUMIN (PIKE, PI 5.0,	COMPLEXED WITH IPVAA 1	TWO CALCIUM IONS	DIFFRACTION) IPVAA 2	CALCIUM-BINDING PROTEIN ALPHA-PARVALBUMIN 1RTP 3	TROPONIN C; CHAIN: NULL;						TROPONIN C; CHAIN: NULL;							TROPONIN C; CHAIN: NULL;
SEQFOL D score					55.26				55,44							89.65							
PMF		0.72	0.80	0.89						0.35													96.0
Verify		0.26	-0.11	0.03						-0.10													-0.13
Psi Blast		9.6c-36	3.2e-34	4.8e-51	1.6e-15				3.2e-16	1.16-30						1.6e-41							1.6e-41
END AA		169	101	691	104				104	101						169							169
STAR T AA		31	_	31	7				7	-						24							33
CHAI N ID		A	A	¥	A				_														
EDB ID		Itp1	lexr	lexr	lpva				함	Itcf						Itcf						,	<u> </u>
SEQ No in		1738	1738	1738	1738				1738	1738						1738						000	1/38

PDB annotation	COVIRACTION, CALCIUM- BINDING, TROPONIN, EF HAND, 2 OPEN CONFORMATION REGULATORY DOMAIN, CALCIUM- REGULATORY DOWALE CONTRACTION	CALCIUM-BINDING PROTEIN EF- HAND ITNX 14	CALCIUM-BINDING PROTEIN EP- HAND ITNX 14	CALCIUM-BINDING PROTEIN BF- HAND 1TNX 14						CALMODULIN, CALCTUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCTUM-BINDING PROTEIN/PEPTIDE)	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2
Coumpound		TROPONIN C; 1TNX 4 CHAIN: NULL; 1TNX 5	TROPONIN C; ITNX 4 CHAIN: NULL; ITNX 5	TROPONIN C; ITNX 4 CHAIN: NULL; ITNX 5	CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 3	CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 3	CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 3	CALCUM BINDING PROTEIN CALMODULIN (TRE-2-C\$ FRAGMENT COMPRISING RESIDUES 78 - 148 1TRC 3 OF THE INTACT MOLECULE) ITRC	MUSCLE PROTEIN TROPONIN C (TRIC FRAGMENT) (APO FORM) (NMR, 1 STRUCTURE) 1TRF 3	CALMÓDULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN; CHAIN: A; RS20; CHAIN: B;
SEQFOL D score			84.53			96.98		62.97	66.58		60.06
PMF		0.41		0.94	0.30		1.00			0.36	
Verify		-0.26		21.0	-0.20		0.13			-0.06	
Psi Blast		9.6e-34	1.6e-38	1.6e-38	3.2e-32	4.8e-42	4.8e-42	.8e-22	3.2e-26	9.6e-36	1.1e-51
END		101	169	169	101	691	169	103	106	104	170
STAR T AA		_	24	33	1	20	33	36	31	-	31
CHAI N ID								∢		∢	4
ED CI		Itmx	1tmx	ltmx	Itop	ltop	Itop	ltre	ltrf	lvrk	lvrk
SEQ No ib		1738	1738	1738	1738	1738	1738	1738	1738	1738	1738

			,				_				
PDB annotation	COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)	CALMODULIN, CALCTUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCTUM-BINDING PROTEIN/PEPTIDE)	MUSCLE PROTEIN MYOSIN, CALCIUM BINDING PROTEIN, MUSCLE PROTEIN	MUSCLE PROTEIN MYOSIN, CALCIUM BINDING PROTEIN, MUSCLE PROTEIN	CALCIUM-BINDING PROTEIN CTINC; CARDIAC, MUSCLE, REGULATORY, CALCIUM-BINDING PROTEIN				TRANSFERASE ATP:AMP- PHOSPHOTRANSFERASE, TRANSFERASE		
Coumpound		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	SCALLOP MYOSIN; CHAIN: A, B, C;	SCALLOP MYOSIN; CHAIN: A, B, C;	TROPONIN C; CHAIN: NULL;	CALCTUM BINDING CALCTUM- BINDING PARVALBUMIN (\$P*1=4.25) 4CPV 3		TRANSFERASE URIDYLATE KINASE (E.C.2.74-) COMPLEXED WITH ADP AND AMP 1UKZ 3	ADENYLATE KINASE; CHAIN: A, B;	TRANSFERASE(PHOSPHOTRA NSFERASE) ADENYLATE KINASE (E.C.2.74.3) 3ADK 4	TRANSFERASE URIDYLATE KINASE (E.C.2.7.4) COMPLEXED WITH ADP AND AMP 1UKZ 3
SEQFOL D score			64.97	54,16	52.43	51.70					
PMF		56:0						0.07	0.13	0.16	0.07
Verify		0.15						-0.05	-0.17	-0.25	-0.05
Psi Blast		1.1e-51	7.5e-26	1.1e-25	8e-10	1.3e-11		0.0006	0.0001	0.0075	0.0006
END AA		169	170	171	<u>\$</u>	103		463	587	495	463
STAR T AA		33	33	33	31	9		362	362	362	362
CHAI N ID		¥	В	O					∢		
PDB ID		lvrk	1wdc	1wdc	3ctn	4сру		lukz	lzak	3adk	lukz
SEQ ID NO:		1738	1738	1738	1738	1738		1745	1745	1745	1746

PDB annotation	TRANSFERASE ATP: AMP. PHOSPHOTRANSFERASE, TRANSFERASE		TRANSFERASE BRUTONS AGAMAAGOBULINEMA TYROSINE KINASE, BTK; TRANSFERASE, PHOMANI, BTK MOTE, ZINC BINDING, X-LINKED 2 AGAMMAGIOBULINEMIA,	1 TRODING-FROLISM LINES. SIGNALING PROTEIN DAPPI, PHISH, BAMA22, PLECKSTRIN, 3- PHOSPHOINOSTILIDES, INOSTOL TETRAKISHPIOSPHATE, 2 SIGNAL TRANSDICTION PROTEIN, ALAPPTOR PROTEIN	SIGNALLING PROTEIN DAPPI, PHISH, BAMA2; FIECKSTEIN, 3-PHOSPITOLISE, INOSITOL, TETRAKISPHOSPHATE 2 SIGNAL TRANSDOUTION PROTEIN, ADAPTOR PROTEIN	SIGNALING PROTEIN ARF1 GUANINE NUCLEOTIDE EXCHANGE FACTOR AND PH DOMAIN	HYDROLASE METALLO-BETA- LACTAMASE, ANTIBIOTIC RESISTANCE, BINUCLEAR 2 ZINC, HYDROLASE
Coumpound	ADENYLATE KINASE; CHAIN: A, B;	TRANSFERASE(PHOSPHOTRA NSFERASE) ADENYLATE KINASE (E.C.2.7.4.3) 3ADK 4	BRUTON'S TYROSINE KINASE; CHAIN: A, B;	DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3- CHAIN: A;	DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3- CHAIN: A;	GRP1; CHAIN: A;	PENICILLINASE; CHAIN: A;
SEQFOL D score							
PMF	0.13	0.16	0.04	0.83	66.0	0.75	-0.14
Verify	-0.17	-0.25	-0.50	0.14	0.25	-0.02	90:08
Psi Blast	0.0001	0.0075	90-39	3e-15	36-16	7.5e-12	1.6e-14
END	587	495	142	142	142	142	178
STAR T AA	362	362	53	55	48	52	8
CHAI	V		· V	∢	∢	A	4
PDB ID	lzak	3adk	16tk	Ifao	1fb8	Ifgy	Isml
SEQ ID NO:	1746	1746	1749	1749	1749	1749	1750

PDB annotation	HYDROLASE HYDROLASE, BETA- LACTAMASE, ANTIBIOTIC, METALLOENZYME	OXIDOREDICTASE OXIDOREDICTASE, METALLOPROTEIN, FE(II) COMPLEX, CATECHOL	OXIDOREDUCTASE OXIDOREDUCTASE, METALLOPROTEIN, FE(II) COMPLEX, CATECHOL	HYDROLASE PHOSPHOLIPASE C:	ZINC PHOSPHOLIPASE C, GANGRENE DETERMINANT. C2	DOMAIN, CA 2 AND MEMBRANE BINDING, HYDROLASE	COMPLEX	(HYDROLASE/COFACTOR)	IRIACYLGLYCEROL LIPASE; COMPLEX	(HYDROLASE/COFACTOR), LIPID DEGRADATION	OXIDOREDUCTASE 15LOX;	OXIDOREDUCIASE, ISLO DEPOIZ	OXIDOREDUCTASE 15LOX; OXIDOREDUCTASE, 15LO DEPOT2	DIOXYGENASE L-1; DIOXYGENASE,	LIPOXYGENASE, METALLOPROTEIN, FATTY ACIDS	DIOXYGENASE L-1; DIOXYGENASE,	LIPOXYGENASE, METALLOPROTEIN, FATTY ACIDS	
Coumpound	METALLO BETA-LACTAMASE II; CHAIN: A, B;	LIPOXYGENASE-3; CHAIN: NULL;	LIPOXYGENASE-3; CHAIN: NULL;	ALPHA-TOXIN; CHAIN; NULL:			TRIACYLGLYCEROL ACYL-	HYDROLASE; CHAIN: A, C;	COLIPASE; CHAIN: B, D		15-LIPOXYGENASE; CHAIN:	NULL;	IS-LIPOXYGENASE; CHAIN: NULL;	LIPOXYGENASE-1; CHAIN:	NOLL;	LIPOXYGENASE-1; CHAIN:	NULL;	
SEQFOL D score		253.58										100.00	482.93	231.83				
PMF	-0.05		1.00	0.04			0.45				1.00					1.00		
Verify	0.18		0.36	-0.01			0.46				0.41					0.18		
Psi Blast	1.6e-14	0	0	1.6e-20		_	0.0045				0			0		0		
END	170	IF .	7117	Ξ			66				711	21.6	-	711		711		
STAR	3	-	35	7			4				2		7	_		46		
CHAI N ID	¥						٧											
10 CI	2bc2	lbyt	lbyt	[ca]			1eth				Ilox	T out	X	1yge		1yge		
SE ON	1750	1751	1751	1751			1751				1751	1761	ē	1751		1751		

Г	_	0		Т		_	_	-	Г		-	Γ		_	Γ								Т	-			_	-		_	Τ		-
PDB annotation		SIGNALING PROTEIN GTP-BINDING PROTEIN RHOA, GTPASE RHOA;	RHO GDI 1; RHO GTPASE, G-	PROTEIN, SIGNALING PROTEIN	SIGNALING PROTEIN GTP-BINDING	PROTEIN RHOA, GTPASE RHOA;	RHO GDI I; RHO GTPASE, G-	PROTEIN, SIGNALING PROTEIN	CELL CYCLE CDC42; RHO GDI 1;	GTP-BINDING PROTEIN, CDC42,	RHOGDI, X-RAY	CELL CYCLE CDC42; RHO GDI 1;	GTP-BINDING PROTEIN, CDC42,	RHOGDI, X-RAY		and the second s																DNA, COMPLEX, DNA-BINDING	PROTEIN, PROTEIN/DNA
Coumpound		TRANSFORMING PROTEIN RHOA; CHAIN: A, C; RHO GDP	DISSOCIATION INHIBITOR	ALPHA; CHAIN: E, F;	TRANSFORMING PROTEIN	RHOA; CHAIN: A, C; RHO GDP	DISSOCIATION INHIBITOR	ALPHA; CHAIN: E, F;	GTP-BINDING PROTEIN;	CHAIN: A; GDP-DISSOCIATION	INHIBITOR 1; CHAIN: B;	GTP-BINDING PROTEIN;	CHAIN: A; GDP-DISSOCIATION	INHIBITOR 1; CHAIN: B;		DNA-BINDING PROTEIN	ANTENNAPEDIA PROTEIN	(HOMEODOMAIN) MUTANT	WITH CYS 39 1AHD 3	REPLACED BY SER (C39S)	COMPLEX WITH DNA (NMR,	1AHD 4 16 STRUCTURES) 1AHD	0	DNA-BINDING PROJEIN	ANIBINAFEDIA FROIEIN	(HUMEUDOMAIN) MUTANT	WILH CIS 39 IAHD 3	NEFLACED BY SEK (L398)	LATID 4 15 STRIPTING (NMK,	S SAMPOLIONES) IARID	HOMEOBOX PROTEIN HOX-BI;	CHAIN: A; PBX1; CHAIN: B;	DNA CHAIN: D; DNA CHAIN: E;
SEQFOL D score																70.63																	
PMF		1.00			I.00				I.00			1.00												0.90							86'0		
Verify		0.50			0.33				0.48			0.48												-0.12							-0.15		
Psi Blast		4.5e-66			9.6e-70				92-a9			1.6e-78				6.4e-36								0.46-30							3e-31		
END		162			177				162			180		-		98								ç							81		_
STAR		24			24				2			5				. 61								3							21		_
CHAI		ш		,	ш				В			В				ы								4		_					Ą		
PDB ID		lcc0			1000				ldoa			Idoa				lahd								Dual				_			1672		
SEQ ID	SO.	1753		1	1753				1753			1753				1757							200	/2/							1757		

40.00					_			_			_		_	_	_		_	_	_	_	_	
PDB annotation	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA	PROTEIN/DNA HOMEODOMAIN, DNA, COMPLEX, DNA-BINDING PROTEIN, PROTEIN/DNA	TRANSCRIPTION/DNA UL/TRABITHORAX, PBX PROTEIN; DNA BINDING, HOMEODOMAIN, HOMEOTIC PROTEINS, DEVELOPMENT, 2 SPECIFICITY		TRANSCRIPTION/DNA	ULTRABITHORAX; PBX PROTEIN;	DNA BINDING, HOMEODOMAIN,	DEVELOPMENT 2 SPECIFICITY														
Coumpound	HOMEOBOX PROTEIN HOX-BI; CHAIN: A; PBXI; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E;	HOMEOBOX PROTEIN HOX-B1; CHAIN: A; PBX1; CHAIN: B; DNA CHAIN: D; DNA CHAIN: E;	ULTRABITHORAX HOMEOTIC PROTEIN IV; CHANI: A; HOMEOBOX PROTEIN EXTRADENTICLE; CHAIN: B; DNA (5- CHAIN: C; DNA (6-	CHAIN: D:	ULTRABITHORAX HOMEOTIC	PROTEIN IV; CHAIN: A;	HOMEOBOX PROTEIN	DNA (5'- CHAIN: C: DNA (5'-	CHAIN: D;	DNA-BINDING FUSHI TARAZU	PROTEIN (HOMEODOMAIN)	DNA-BINDING FUSHI TARAZU	PROTEIN (HOMEODOMAIN)	(NMR, 20 STRUCTURES) IFTZ 3	DNA-BINDING PROTEIN OCT-1	DNA-BINDING PROTEIN	ANTENNAPEDIA PROTEIN	(HOMEODOMAIN) MUTANT	WITH CYS 39 ISAN 3	REPLACED BY SER AND	RESIDUES 1-6 DELETED	(C39S,DEL 1-6) ISAN 4 (NMR, 20 STRUCTURES) ISAN 5
SEQFOL D score		64.24	64.34							66.44						69.69						
PMF	66.0				0.82							0.81			0.23							
Verify score	0.19				-0.14							-0.01			-0.70							
Psi Blast	3.2e-28	3e-31	6.4e-31		6.4e-31					4.8e-32		4.8e-32			3e-31	1.6e-33						
END		18	11		78					98		85			92	98						
STAR T AA	24	6	20		2					18		19		I	_	25						
CHAI N ID	∢	V	∢		A										υ							
PDB CI	1672	1672	168i		1881					11/12		Iftz		7	Joet	Isan						
SEQ NO.	1757	1757	1757		1757					1757		1757			1757	1757						

PDB annotation		COMPLEX (DNA-BINDING PROTEIN/DNA) HD; HOMEODOMAIN, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) HD; HOMEODOMAIN, COMPLEX (DNA-BINDING PROTEIN/DNA)	LIPOCALIN LIPOCALIN, OLFACTION	SUGAR BINDING PROTEIN NGAL; NEUTROPHIL, NGAL, LIPOCALIN	ALLERGEN LIPOCALIN, BETA BARREL			ODORANT-BINDING PROTEIN OBPOLFACTION, NOSE, TRANSPORT, LIPOCALIN, ODORANT-BINDING 2
Coumpound	DNA-BYDDIA PROTEIN ANTENIA-PEDIA PROTEIN (HOMEODOMAIN) MUTANT TYS DIANT CYS DI SAN 13 REPLACED BY SER AND RESIDUES 1-6 DELETED STRUCTURES 15AN 5 STRUCTURES 15AN 5	ANTENNAPEDIA PROTEIN; CHAIN: A, B; DNA; CHAIN: C, D, E, F;	ANTENNAPEDIA PROTEIN; CHAIN: A, B; DNA; CHAIN: C, D, E, F;	ODORANT BINDING PROTEIN; CHAIN: A, B;	HUMAN NEUTROPHIL GELATINASE; CHAIN: A, B;	ALLERGEN EQU C 1; CHAIN: A;	PHEROMONE-BINDING MAJOR URINARY PROTEIN COMPLEX WITH 2-(SEC-BUTYL,) IMUP 3 THIAZOLINE IMUP 4	PHEROMONE-BINDING MAJOR URINARY PROTEIN COMPLEX WITH 2-(SEC-BUTYL) IMUP 3 THIAZOLINE IMUP 4	ODORANT-BINDING PROTEIN; CHAIN: A, B;
SEQFOL D score			68.97					64.35	
PMF	86:0	00:1		98.0	1.00	0.95	1:00		-0.02
Verify score	-0.17	-0.13		0.63	99.0	0.00	0.78		0.19
Psi Blast	1.60-33	1.6e-33	1.6e-33	3e-35	4.5e-47	1.4e-38	6e-37	6e-37	9e-36
END	82	79	79	691	691	691	891	891	172
STAR T AA	26	24	24	38	20	30	25	25	30
CHAI N ID		<	4	A	<	A			A
EDB CI	lsan	9ant	9ant	la3y	Idfv	Iew3	lmup	Imup	lobp
SEQ No B	1757	1757	1757	1758	1758	1758	1758	1758	1758

PDB annotation	PROTEIN	SUGAR BINDING PROTEIN NGAL; NEUTROPHIL LIPOCALIN, SIGNAL PROTEIN, GLYCOPROTEIN		LIPID BINDING PROTEIN A2U- GLOBULIN, LIPID BINDING PROTEIN	LIPID BINDING PROTEIN A2U- GLOBULIN, LIPID BINDING PROTEIN	LIPID BINDING PROTEIN A2U. GLOBULIN, LIPID BINDING PROTEIN	COMPLEX (VIRAL CAPSID/IMMUNOGLOBULIN) HIV-1 CA, HIV CA, HIV P24, P24; FAB, FAB	LIGHT CHAIN, FAB HEAVY CHAIN COMPLEX (VIRAL	CAPSID/IMMUNOGLOBULIN), HIV, CAPSID PROTEIN, 2 P24	COMPLEX (MHC/VIRAL	HEAVY CHAIN; CLASS I MHC, T-	CELL RECEPTOR, VIRAL PEPTIDE, 2	COMPLEX (MHC/VIRAL	IMMUNOGLOBULIN HUMAN FAB,	ANTI-TETANUS TOXOID, HIGH	AFFINITY, CRYSTAL 2 PACKING MOTIF, PROGRAMMING
Coumpound		NEUTROPHIL GELATINASE; CHAIN: A;	RETINOL TRANSPORT RETINOL BINDING PROTEIN IRBP 3	ALPHA-2U-GLOBULIN; CHAIN: A, B, C, D	ALPHA-2U-GLOBULIN; CHAIN: A, B, C, D	ALPHA-2U-GLOBULIN; CHAIN: A, B, C, D	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 CAPSID CHAIN: A, B; ANTIBODY FAB25.3	FRAGMENT; CHAIN: H, K, L, M;		HLA-A 0201; CHAIN: A; BETA-2	TAX PEPTIDE; CHAIN: C; T	CELL RECEPTOR ALPHA;	CHAIN: D; T CELL RECEPTOR RETA: CHAIN: F:	FAB B7-15A2; CHAIN: L, H;		
SEQFOL D score						78.30				295.76						
PMF		1.00	-0.09	66'0	1.00		1.00							1.00		
Verify score		0.83	0.14	69:0	16.0		0.30							0.48		
Psi Blast		4.5e-40	le-35	1.3e-36	1.5e-37	1.5e-37	1.6e-94			4.8c-64				1.6e-95		
END		169	168	169	691	691	249			263				252		
STAR T AA		17	26	25	25	25	5			77				22		
CHAI N ID		¥		A	Ą	Ą	I			ш				H		
FDB 61		lqqs	1rbp	2a2u	2a2u	2a2u	lafv			lao7				1aqk		
SEQ NO:		1758	1758		1758	1758	1759			1759				1759		

					_					_	_	_	_		_	_			_	_		_		_	_	
PDB annotation	PROPENSITY TO CRYSTALLIZE, 3 IMMUNOGLOBULIN	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA A2	HEAVY CHAIN; COMPLEX	(MITC) VINCE LES LIDENECES LON)	Cost Of the Carrie and the Co	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA A2	HEAVY CHAIN; COMPLEX	(MHC/VIRAL PEPTIDE/RECEPTOR)							CATALYTIC ANTIBODY	CATALYTIC ANTIBODY 6D9	CATALYTIC ANTIBODY, ESTER	HYDROLYSIS, ESTEROLYTIC, FAB, 2 IMMUNOGLOBULIN							IMMI NOGI OBIII IN INTACT	IMMUNOGLOBULIN V REGION C
Coumpound		HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B;	TAX PEPTIDE; CHAIN: C; T	CHAIN: D; T CELL RECEPTOR	BEIN, CHAIN: E;	HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B;	TAX PEPTIDE; CHAIN: C; T	CELL RECEPTOR ALPHA;	CHAIN: U; I CELL KECEPTOR BETA: CHAIN: E:	IMMUNOGLOBULIN 3D6 FAB	1DFB 3	IMMUNOGLOBULIN FAB	FRAGMENT OF HUMANIZED	ANTIBODY 4D5, VEKSION 4 1FVD 3	IMMUNOGLOBULIN 6D9;	CHAIN: L, F;			COMPLEX	(ANTIBODY/BINDING	PROTEIN) IGGI FAB	FRAGMENT COMPLEXED	WITH PROTEIN G (DOMAIN III)	HGC 5 PROTEIN G,	IGG2A INTACT ANTIBODY -	MAB231; CHAIN: A, B, C, D
SEQFOL D score					00000	386.70																				
PMF		1.00								1.00		1.00			1.00				1.00						00 0	
Verify		0.74								0.30		0.41			0.47				0.21						0.42	-
Psi Blast		1.2e-98			1 30 00	75-98 1.76-98				9.6e-94		6.4e-96			4.8c-95				I,6e-95						86-99	
END AA		263			200	507				252		252			252				252						263	
STAR T AA		22			60	77				21		21			21				22						21	
CHAI		ы				2]				H		Д			Ξ				E						20	,
PDB ID		1bd2			5	Tpq7				1dfb		1fvd	_		1hyx				lige						id	b
SEQ NO.		1759			1760	66/1				1759		1759			1759				1759						1759	

PDB annotation	REGION, IMMUNOGLOBULIN	IMMUNOGLOBULIN,	COOPPLES (MAMUNOCIOBULN, IGGI, FAB MAMUNOCIOBULN, IGGI, FAB FREAGMENT, CROSS-REACTIVITY, HIVI PROTEASE, ENZYME 2 (MAMUNOCIOBULN/PEPTIDE)	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, PROFEDTOR FNZYME INHIBITION	GLA, EGF, 3 COMPLEX (SERINE	PROTEASE/COFACTOR/LIGAND)	PLANT PROTEIN TWO HOMOLOGOUS HEVEIN-LIKE	S	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN	SUGAR BINDING PROTEIN UDA;	LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN, SACCHARIDE		SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN	BLOOD COAGULATION INHIBITOR
	REGION,	IMMUNO	COMPLEX (IMMUNOO IMMUNOC FRAGMEN HIVI PROT INHIBITIO	BLOOD C PROTEAS	GLA, EGF	PROTEAS	PLANT PF HOMOLO	DOMAINS	SUGAR BINDING LECTIN, HEVEIN SUPERANTIGEN	SUGAR B.	SUPERAN	BINDING	SIGNALLI PROTEIN, PROTEIN	PROTEIN, PROTEIN,	BLOODC
Coumpound		N1G9 (IGG1=LAMBDA=); CHAIN: L, H;	MONOCLONAL ANTIBODY F11.23; CHAIN: L, H, M, HIV.1 PROTEASE PEPTIDE; CHAIN: P, Q;	BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLIBLE TISSIE FACTOR:	CHAIN: T, U, D-PHE-PHE-ARG-	CHLOROMETHYLKETONE (DFFRCMK) WITH CHAIN: C;	AGGLUTININ ISOLECTIN VI; CHAIN: A		AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V; CHAIN: A:	AGGLUTININ ISOLECTIN	I/AGGLUTININ ISOLECTIN V/ CHAIN: A;		TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	FLAVORIDIN; 1FVL 4 CHAIN:
SEQFOL D score				50.68					,				62.34		
PMF		1.00	1.00				0.01		-0.12	0.00				0.36	0.04
Verify score		0.35	0.39				0.40		90.0	-0.20				-0.34	-0.37
Psi Blast		1.6e-93	3.2e-93	6e-10			1.1e-07		3e-08	60-a9			3e-12	3e-12	1.2e-12
END		249	251	195			88		8	88			192	203	10I
STAR T AA		21	22	64			12		22	12			37	57	31
CHAI		н	Н	1			∢.		¥	¥			∢	V	
FDB TD		dBul	2hrp	Idan			lehd		leis	Ien2			lext	lext	Iţ.
SEQ NO.		1759	1759	1762			1762		1762	1762	_		1762	1762	1762

			_				_			_					_	_	_		_		-	_	_	_	_	_	_		_
PDB annotation	GP IIB/IIIA ANTAGONIST 1FVL 9	GLYCOPROTEIN GLYCOPROTEIN	GLYCOPROTEIN GLYCOPROTEIN	SIGNALLING PROTEIN TYPE I RECEPTOR, STNFRI: INCF 8	BINDING PROTEIN, CYTOKINE	SIGNALLING PROTEIN TYPE I	RECEPTOR, STNFRI; INCF 8	BINDING PROTEIN, CYTOKINE INCF 19	COMPLEX (BLOOD	CHRISTMAS FACTOR; COMPLEX,	INHIBITOR, HEMOPHILIA/EGF,	BLOOD COAGULATION, 2 PLASMA,	SERINE PROTEASE, CALCIUM-	BINDING, HYDROLASE, 3	OPT COLUMN	SERINE PROTEASE INHIBITOR	FACTOR XA INHIBITOR,	ANTISTASIN, CRYSTAL	STRUCTURE, FACTOR XA	INHIBITOR, 2 SERINE PROTEASE	STRING ON, I HIKOMBOSIS	SEKINE PROTEASE INHIBITOR	PACION AN INHIBITOR;	ANTISTASIN, CRYSTAL	STRUCTURE, FACTOR XA	INHIBITOR, 2 SERINE PROTEASE	INTERLIOR, IEROMBOSIS	SERINE PROTEASE INHIBITOR	ANTISTASIN, CRYSTAL
Coumpound	NULL IFVL 5	LAMININ; CHAIN: NULL;	LAMININ; CHAIN: NULL;	TUMOR NECROSIS FACTOR RECEPTOR: 1NCF 4 CHAIN: A.	B; INCF 5	TUMOR NECROSIS FACTOR	RECEPTOR; INCF 4 CHAIN: A,	B; INCF 5	FACTOR IXA; CHAIN: C, L.; D- PHE-PRO-ARG; CHAIN: I:	-					Total Control Control Control	ANTISTASIN; CHAIN: NULL;					ANEMOTA SIM. OLIANI, MILLI	ANTISTASIN; CHAIN: NULL;					The state of the s	ANTISTASIN; CHAIN: NULL;	
SEQFOL D score			66.44			55.28			57.36												60 37	60.00							
PMF		-0.12		0.23											0.10	0.15											9	0.12	
Verify score		0.17		-0.24											200	0.05												-0.14	
Psi Blast		4.5e-19	1.3e-20	7.5e-09		7.5e-11			3e-14						12	3e-17					150.10	01-20-10					01.0	26-18	
END		184	203	140		189			176						-	171					161	ī					121	70	
STAR T AA		15	48	17		55			41						91	19					63	·					05	28	
CHAI N ID				¥		A			J				_														ĺ		
PDB ID		1Klo	Iklo	Incl		Incf			βď						Tolen	ISKZ					1047	TOUT			_		Toler	ISKZ	
SEQ ID NO:		1762	1762	1762		1762			1762						1760	70/1					09/1	7/07					1760	70/1	

PDB annotation	STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; AVISTASIN, CRYSTAL, STRUCTURE, FACTOR XA INHIBITOR, 7.3 SERINE PROTEASE INHIBITOR, THROMBOSIS		TREFOIL FAMILY OF PEPTIDES PSP REPEAT, GROWTH FACTOR, SIGNAL			SIGNAL TRANSDUCTION PROTEIN	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS	
Coumpound		ANTISTASIN; CHAIN: NULL;	MEMBRANE PROTEIN VITELLINE MEMBRANE OUTER LAYER PROTEIN I IVMO 3	PORCINE PANCREATIC SPASMOLYTIC POLYPEPTIDE; CHAIN: A, B;	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	BETA-SPECTRIN; 1BTN 4 CHAIN: NULL: 1BTN 5	SYNAPTOTAGMIN'I, CHAIN: A,	SYNAPTOTAGMIN I; CHAIN: A;
SEQFOL D score				61.72		97.20			
PMF score		80.0-	-0.15		0.13		0.70	0.24	0.01
Verify score		0.13	0.36		0.12		-0.02	0.52	0.04
Psi Blast		4.5e-17	9e-33	0.0014	1.5e-18	6e-29	0.003	0.0043	1.2e-11
END		204	190	191	133	191	234	347	349
STAR T AA		86	35	8	13	32	200	245	245
CHAI N ID			Ą	V	A	A		4	A
PDB TD		Iskz	lvmo	2psp	9wga	9мgа	1btn	lbyn	1byn
SEQ No ib		1762	1762	1762	1762	1762	1768	1768	1768

PDB annotation	ENDOCYTOSIS/EXOCYTOSIS	SANDWICH, CALCIUM ION, C2 DOMAIN	SIGNALING PROTEIN DAPPI, PHISH, BAMAS, PLECKSTEIN, 3- PHOSPHOINOSITIDES, INOSITIOL TETRAKISPHOSPHATE 2 SIGNAL TRANSDUCTION PROTEIN,	ADATOR RROTEN GRALLING PROTEN DAPPI, PHISH, BAM32; PLECKSTRIN, 3- PHOSPHONOSTIDES, INOSITOI. TETRAKISPHOSPHATE, SIGNAL TRANSDUCTION PROTEIN,	ADATOR FOUR DEPOTENT NET 333; NEUROFIBROALIN TYPE I NEUROPIBROALIN TANE I SAL 2 SIGNAL TRANSDICTION, CANCER, GROWTH REGULATION, GIN SHOROLY STANSSING PATENT (OFF 3 FYDROLY NESS), PATENT (OFF 3 FYDROLY NESS), PATENT		
Coumpound		SYNAPTOTAGMIN III; CHAIN: A;	DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3- CHAIN: A;	DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3- CHAIN: A;	NEUROFIBROMĪN; CHAIN: A;	NEUROFIBROMIN; CHAIN: <i>A</i> ş	PHOSPHORYLATION PLECKSTRIN (N-TERMINAL PLECKSTRIN HOMOLOGY
SEQFOL D score					108.36		
PMF		0.54	0.36	0.70		0.99	0.37
Verify		0.47	0.07	-0.29		0.21	0.33
Psi Blast		4.5e-05	6e-05	9e-06	7.5e-68	7.5e-68	4.5e-05
END		362	235	239	687	682	239
STAR T AA		247	173	173	400	416	173
CHAI N ID		V	<	<	∢	<	
PDB ID		1dqv	Ifao	Ifb8	Infl	Infl	1pls
SEQ No. 13		1768	1768	1768	1768	1768	1768

PDB annotation		SIGNAL TRANSDUCTION SON OF SEVENLESS, PLECKSTRIN, SON OF SEVENLESS, SIGNAL TRANSDUCTION	SIGNAL TRANSDUCTION IRS-1; BETA-SANDWHICH, SIGNAL TRANSDUCTION	HYDROLASE CALB DOMAIN; HYDROLASE, C2 DOMAIN, CALB DOMAIN			GTPASE ACTIVATION GAP-334, GAPETTE; GTPASE ACTIVATION, RAS, GAP, SIGNAL TRANSDUCTION, GROWTH 2 REGILATION, CANCER	GTPASE ACTIVATION GAP-334, GAPETTE; GTPASE ACTIVATION, RAS, GAP, SIGNAL TRANSDUCTION, GROWTH 2 REGULATION, CANCER	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA
Coumpound	WITH LEU GLU (HIS)6 ADDED TO THE C TERMINUS IPLS 4 (INS(G105-LEHHHHHH)) (NMR, 25 STRUCTURES) IPLS 5	SOS 1; CHAIN: NULL;	INSULIN RECEPTOR SUBSTRATE 1; CHAIN: A, B;	PHOSPHOLIPASE A2; CHAIN: NULL;	CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2	CALCIUM/PIONED BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) 1RSY 3	P120GAP; CHAIN: NULL;	P120GAP; CHAIN: NULL;	SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'- R(P*GP*UP*UP*UP*
SEQFOL D score								183.05	
PMF		0.39	0.16	0.22	0.05	0.49	1.00		-0.19
Verify		-0.48	0.17	0.22	-0.14	0.13	0.62		0.05
Psi Blast		0.00015	30-05	90-99	0.0043	1.5e-09	1.5e-91	1.50-91	3.2e-14
END		235	245	349	347	349	712	718	205
STAR T AA		162	184	247	245	246	397	397	126
CHAI N ID			A						A
PDB ID		Ipms	app1	lriw	Irsy	lrsy	lwer	lwer	1b7f
SEQ NO:		1768	1768	1768	1768	1768	1768	1768	1770

		A TRA	4, RNA	A TRA		I, RNA	A TRA		I, RNA		JLY(A)	I; RRM,	ENE				JLY(A)	1; RRM,	ENE				JLY(A)	I; KKM,	ENE			(A)T(A)	RRM
PDB annotation	COMPLEX	RNA-BINDING PROTEIN/RN PRE-MRNA: SPLICING	REGULATION, RNP DOMAIN, RNA	RNA-BINDING PROTEIN/RNA TRA	PRE-MRNA; SPLICING	REGULATION, RNP DOMAIN, RNA	RNA-BINDING PROTEIN/RNA TRA	PRE-MRNA; SPLICING	REGULATION, RNP DOMAIN, RNA	COMPLEX	GENE REGULATION/RNA POLY(A)	BINDING PROTEIN 1, PABP 1; RRM,	PROTEIN-RNA COMPLEX, GENE	REGULATION/RNA			GENE REGULATION/RNA POLY(A)	BINDING PROTEIN 1, PABP 1; RRM,	PROTEIN-RNA COMPLEX, GENE	REGULATION/RNA			GENE REGULATION/RNA POLY(A)	BINDING PROTEIN 1, PABP 1; KKM,	FROIDIN-KINA COMPLEA, GENE	KEGULATION/KNA		GENE REGULATION/RNA POLY(A)	BINDING PROTEIN 1. PABP 1: RRM.
Coumpound	UP*UP*UP*UP*U)- CHAIN: P, Q;	SXL-LETHAL PROTEIN; CHAIN: RNA-BINDING PROTEIN/RNA TRA	R(P*GP*UP*UP*GP*UP*UP*UP* UP*UP*UP*UP*U-CHAIN: P. O:	SXL-LETHAL PROTEIN; CHAIN:	A, B; RNA (5'-	R(P*GP*UP*UP*GP*UP*UP*UP*	SXL-LETHAL PROTEIN: CHAIN:	A, B; RNA (5'-	R(P*GP*UP*UP*GP*UP*UP*	UP*UP*UP*UP*U)- CHAIN: P, Q;	POLYDENYLATE BINDING	PROTEIN 1; CHAIN: A, B, C, D,	E, F, G, H; RNA (5'-	R(*AP*AP*AP*AP*AP*AP*	AP*AP*AP*A)-3'); CHAIN: M, N,	O, P, Q, R, S, T;	POLYDENYLATE BINDING	PROTEIN 1; CHAIN: A, B, C, D,	E, F, G, H; RNA (5'-	R(*AP*AP*AP*AP*AP*AP*	AP*AP*AJ-3'); CHAIN: M, N,	O, P, Q, K, S, 1;	POLYDENYLATE BINDING	FROIBIN I; CHAIN: A, B, C, D,	E, F, G, H; NIVA (3-	K("AP"AP"AP"AP"AP"AP"	AP"AP"AP"A); CHAIN: M, N,	POLYDENYLATE BINDING	PROTEIN 1: CHAIN: A. B. C. D.
SEQFOL D score																													
PMF		-0.02		1.00			0.51				-0.01						98.0					1						68'0	
Verify		0.24		0.63			0.63				60.0						0.40					000	0.0					0.45	
Psi Blast		1.6e-37		4.8e-34			4.8e-14				1.6e-39						6.4e-34						1.06-32					6.4e-28	
END		314		425			431				320						431					000	99					409	
STAR		132		236			348				136						238					361	001					238	
CHAI N ID		¥		A			Ą				V						٧					-	α					В	
PDB		J291		1b7f			1b7f				lcvj						levj						Tcv]					Icvj	
SEQ NO.		0221		1770			1770				1770						1770					0001	2//1					1770	

PDB annotation	REGULATION/RNA	GENE REGULATIONRNA POLY(A) BINDING PROTEIN, I, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATIONRNA	GENE REGULATION/RNA POLY(A) BINDING PROTEIN I, PABE I; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	GENE REGULATIONRNA POLY(A) BINDING PROTEIN I, PABP I; RRM, PROTEIN-RANA COMPLEX, GENE REGULATION/RNA	GENE REGULATIONRAA POLY(A) BINDING PROTEIN I, PABI 1; RRA, PROTEIN-RAA COMPLEX, GENE REGULATIONRAA	RNA BINDING PROTEIN RNA- BINDING DOMAIN	RNA BINDING PROTEIN RNA- BINDING DOMAIN	RNA BINDING PROTEIN RNA- BINDING DOMAIN	RNA BINDING PROTEIN RNA-
Coumpound	R(*AP*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*	POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP* O, P, Q, R, S, T;	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP* O, P, Q, R, S, T, O, P, Q, R, S, T,	POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*Al*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP* O, P, Q, R, S, I, Q, R, S, P, R, P, Q, R, S, P, Q, R, S, P, R, P, R, P,	HU ANTIGEN C; CHAIN: A;	HU ANTIGEN C; CHAIN: A;	HU ANTIGEN C; CHAIN: A;	HU ANTIGEN C: CHAIN: A;
SEQFOL D score									
PMF		0.76	0.65	0.25	0.68	0.19	0.27	-0.19	-0.03
Verify		0.33	0.17	0.03	0.78	0.04	0.52	0.03	0.48
Psi Blast		1.6e-12	6.4e-21	1.6e-21	1.6e-12	3.20-21	4.8e-13	8e-14	3.2e-18
END AA		435	402	405	435	322	431	218	319
STAR T AA		352	238	238	352	233	346	136	237
CHAI		д	CE-q	н	Н	V	٧	Ą	Ą
PDB DD		lcvj	levj	lcvj	levj	z8p1	Z8P1	149a	1d9a
SEQ NO IB		1770	1770	1770	0221	0221	1770	1770	1770

PDB annotation	BINDING DOMAIN	RIBONUCLEOPROTEIN UI A117; RIBONUCLEOPROTEIN, RNP	DOMAIN, SPLICEOSOME	STRUCTURAL PROTEIN PROTEIN	C23; RNP, RBD, RRM, RNA BINDING DOMAIN, NUCLEOLUS	NUCLEAR PROTEIN	HETEROGENEOUS NUCLEAR	RIBONUCLEOPROTEIN A1,	NUCLEAR PROTEIN, HNRNP, RBD,	RRM, RNP, RNA BINDING, 2	NUCLEAR PROTEIN	HETEROGENEOUS NUCLEAR	RIBONUCLEOPROTEIN A1,	NUCLEAR PROTEIN, HNRNP, RBD,	RRM, RNP, RNA BINDING, 2	RIBONUCLEOPROTEIN	NUCLEAR PROTEIN	HETEROGENEOUS NUCLEAR	RIBONUCLEOPROTEIN A1,	NUCLEAR PROTEIN, HNRNP, RBD,	RRM, RNP, RNA BINDING, 2	RIBONUCLEOPROTEIN	RNA BINDING PROTEIN RNA-	BINDING DOMAIN		RNA BINDING PROTEIN RNA-	SINDING DOMAIN		RNA BINDING PROTEIN RNA- BINDING DOMAIN	
Coumpound		LEAR ROTEIN A;		NUCLEOLIN RBD2; CHAIN: A; S		HNRNP A1; CHAIN: NULL;			_	-	HNRNP AI; CHAIN; NULL;	_			-		HNRNP A1; CHAIN: NULL;	1	1	_	-	┪	K.	EOPROTEIN D0;	1	4	EOPROTEIN DO;	CHAIN: A;	HETEROGENEOUS NUCLEAR RIBONI (CLEOPROTEIN DO:	_
SEQFOL D score																														
PMF		0.12		0.07		-0.09					0.95						0.94						-0.19			91.0			89.0	
Verify		0.57		0.30		0.17					0.21						0.83						0.03			0.78			0.91	
Psi Blast		1.6e-11		3.2e-12		4.8e-45					1.6e-40						1.3e-16						6.4e-20			4.8e-22			9.6e-15	
END AA		315		313		314					425						431						213			314			425	
STAR T AA		230		222		129					231						320						13e			237			351	
CHAI N ID				¥																			<			K			<	
PDB ID		1Br		ığı		Ihal					lhal						[ha]						[pq]			[pq]			Ibdi	
SEQ ID NO:		1770		1770		1770					1770						0/41						1770		0000	1770			1770	

								·	_
PDB annotation	RIBONUCLEOPROTEIN PTB. PTB. C198, HETEROGENEOUS NUCLEAR POLYPYRIMIDNE TRACT BINDING PROTEIN, RNP, RNA, SPICING, 2 TRANSLATION			RNA BINDING PROTEIN RNA- BINDING DOMAIN	RNA BINDING PROTEIN RNA- BINDING DOMAIN	RNA BINDING PROTEIN RNA- BINDING DOMAIN	RNA-BINDING DOMAIN RNA- BINDING DOMAIN, ALTERNATIVE SPLICING	RNA-BINDING DOMAIN RNA- BINDING DOMAIN, ALTERNATIVE SPLICING	_
Coumpound	POLYPYRIMIDINE TRACT- BINDING PROTEIN; CHAIN: A;	RNA-BINDING PROTEIN SEX- LETHAL ROTEIN (C. TERMINUS, OR SECOND RNA- BINDING DOMAIN 18X1.3 (RBD-2), RESIDUES 99-294 PLUS N-TERMINAL MET) 18XL 4 (NMR, 17 STRUCTURES) 18XL	RNA-BINDING PROTEIN SEX- LETHAL ROTEIN (C TERMINUS, OR SECOND RNA- BINDING DOMAKIN 1 SXL, 3 (RBD-2), RESIDIES 195-294 PLUS N-TERMINAL MET) 1 SXL 4 (NMK, 17 STRUCTURES) 1 SXL	MUSASHII; CHAIN: A;	MUSASHII; CHAIN: A;	MUSASHII; CHAIN: A;	SEX-LETHAL PROTEIN; CHAIN: NULL;	SEX-LETHAL PROTEIN; CHAIN: NULL;	SPLICING FACTOR U2AF 65 KD
SEQFOL D seore									
PMF	0.15	-0.15	0.13	-0.18	0.17	66'0	0.25	0.70	0.88
Verify	0.06	0.21	0.51	0.11	0.74	16:0	0.36	0.42	0.75
Psi Blast	4.8e-19	1.6c-18	3.2e-13	1.3e-14	6.4e-19	4.80-14	1.1e-19	4.8e-14	6.4e-18
END	427	319	429	213	314	425	322	431	314
STAR T AA	238	223	341	136	237	351	236	348	236
CHAI	4			<	A	A			Ą
ED CI	1qm9	IX.	lsxl	2mss	2mss	2mss	2sxl	2sxl	2u2f
SEQ Se S	1770	1770	1770	1770	1770	1770	1770	1770	1770

PDB annotation	U2 SNRNP, RBD, RNA-BINDING PROTEIN	COMPLEX (RIBONUCLEOPROTEINDNA) HNRIP AI, UPI, COMPLEX (RIBONUCLEOPROTEINDNA), HETTEROGENEOUS NUCLEAR2	RIBONUCLEOPROTEIN A I COMPLEX (RIBONUCLEOPROTEINDNA) HNRIPA LLOPI, COMPLEX (RIBONUCLEOPROTEINDNA) HFTEROGENEOUS NUCLEAR 2	AIBO WOLZEDOW LIEIN ALI READ BINDING DOMAIN, RBD, RNA RECOGNITON MOTOR, RRA, 2 SPLICING INHBITOR, SEX.3 TRANSLATIONAL INHBITOR, SEX.3 DETRANSLATIONAL INHBITOR, SEX.3 DETRANSLATIONAL INHBITOR, SEX.3 DETRANSLATIONAL INHBITOR, SEX.3	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA BECGNITION MOTIE, RBA, 2 SPLCING INHBITOR, IRANSLATIONAL INHBITOR, DETERMINATION, CCHROMOSOME DOSAGE COMPRINATION	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) ZINC
Coumpound	SUBUNIT; CHAIN: A;	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A.I; CHAIN: A.12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A: 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	SEX-LETHAL; CHAIN: A, B, C;	SEX-LETHAL; CHAIN: A, B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE: CHAIN: B. C.	DNA; CHAIN: A, B, D, E;
SEQFOL D score						74.27	
PMF		60:0	0.52	-0.02	96.0		0.04
Verify		0.00	0.60	0.22	0.32		-0.22
Psi Blast		4.8e-47	1.6e-43	3.2e-36	1.40-32	3.2e-31	9.6e-44
END		319	433	307	425	445	219
STAR		128	231	133	236	363	138
CHAI N ID		∢	<	4	∢.	∢	S
PDB		2up1	2up1	3sxl	3sxl	lalh	1mey
SEQ NO:		0/41	1770	1770	1770	1772	1772

PDB annotation	JER FINGER, PROTEIN-DNA G, INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC PINGERDNA)				COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA G; INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)		~
Coumpound	CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC PINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;
SEQFOL D score							
PMF		0.96	00'1	00'1	1.00	00'1	1.00
Verify		0.35	0.14	0.54	0.24	0.71	0.74
Psi Blast		4.8e-46	4.8c-47	1.3e-47	3.2e-48	1.1e-49	3.2e-50
END		247	275	303	331	359	387
STAR T AA		166	194	222	250	278	306
CHAI N ID		ပ	ن ن	ပ	ပ	o	ပ
PDB ID		Imey	Imey	lmey	Imey	Imey	lmey
SEQ NO:		1772	1772	1772	1772	1772	1772

80 E	CHAI	STAR T AA	END	Psi Blast	Verify score	PMF	SEQFOL D score	Coumpound	PDB annotation
1mey	o	334	415	1.6e-51	0.69	1.00		DNA; CHAIN: A, B, D, E; CONSENGUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGERDNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX
Imey	o	362	443	4.8c-51	-0.02	1.00		DNA; CHAIN: A. B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGERDINA) ZINC COMPLEX (ZINC FINGERDINA) ZINC FINGER, PROTEIN-DINA INTERACTION, PROTEIN DESIGN, 2 CONFERS TOTAL STRUCTURE, COMPLEX COM
Imey	O .	390	471	9.6e-51	0.37	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC PINGERDNA) ZINC COMPLEX (ZINC PINGERDNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER DNA)
Imey	o .	418	499	1.6e-50	0.52	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGERDNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGERDNA)
Imey	O	446	527	1.6e-50	0.31	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGERDNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGERDNA)
Imey	o	446	528	1.6e-50			102.60	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGERDNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGERDNA)
Imey	0	474	531	6.4e-34	0.09	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX

PDB annotation	(ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA NTERACTION, PROTEIN DESIGN, 2 CYSTALS TRUCTURE, COMPLEX (ZINC FINGER DNA)	COMPLEX (TRANSCRIPTION REGULATIONDAN) COMPLEX (TRANSCRIPTION) REGULATIONDANA), RNA POLYMERASE III, 2 PRANSCRIPTION INITIATION, ZINC FRANSCRIPTION INITIATION, ZINC FRANSCRIPTION INITIATION, ZINC	COMPLEX (TRANSCRIPTION REQUIL ATTONOMA) COMPLEX (TRANSCRIPTION) REQUIL ATTONOMA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FENGER PROTEIN	COMPLEX (TRANSCRUTION REGULATION/DNA) COMPLEX (TRANSCRUTION) REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRUTION INITIATION, ZNC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX
Coumpound	DNA; CHAIN: A. B. D. E. CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	TFIIIA; CHAIN: A, D; SS RIBOSOMAL RIVA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; SS RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; SS RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 58 RIBOSOMAL RNA GENE;
SEQFOL D score						100.49
PMF	0.05	0.29	0.54	0.96	0.99	
Verify	0.55	-0.73	0.24	0.28	0.07	
Psi Blast	9.6e-11	1.66-09	1.3e-35	4.8e-37	3.2e-38	3.2e-38
END	161	17.	312	368	452	497
STAR T AA	164	4	167	223	307	334
CHAI N ID	Ð	o	4	4	A	4
PDB	Imey	Imey	91112	911	116	911
SEQ ID NO:	1772	1772	2771	1772	1772	1772

PDB annotation	(TRANSCRIPTION REGULATIONDNA), RNA POLYMERASB III, 2 TRANSCRIPTION INTIATION, ZINC FINGER PROTEIN	COMPLIANT (TRANSCRIPTION REGULATIONIDANS) COMPLEX (TRANSCRIPTION) REGULATIONIDANS), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLIAR (TRANSCRIPTION REGULATIONDNA) COMPLEX (TRANSCRIPTION) REGULATIONDNA), RNA POLYMIRA SE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRETTON REGULATIONDNA) YING-YANG I; TRANSCRETON INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DIAA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRETION)	COMPLEX (TRANSCEPTON) REGULATION/DNA) YING-YANG I; TRANSCERPTION INITIATION, INITIATION, FINESTRY YYI, ZINC 2 FINESTR REQUEST, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCEPTION)
Coumpound	CHAIN: B, C, B, F;	TFIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIA; CHAIN: A, D; 58 RIBOSOMAL, RNA GENE; CHAIN: B, C, B, F;	VYI; CTANN: C; ADBNO- ASSOCIATED VIRUS PS INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS PS BITIATOR ELEMENT DNA; CHAIN: A, B;
SEQFOL D score					
PMF		0.95	0.94	0.11	0.72
Verify		-0.06	0.01	0.07	-0.21
Psi Blast		1.6e-37	1.4e-36	4.88-32	1.5e-23
END		206	529	247	275
STAR T AA		363	166	143	169
CHAI N ID		¥.	A	o	υ
PDB ID		11f6	1116	lubd	1ubd
SEQ NO:		1772	1772	1772	1772

PDB annotation	REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG I; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YYI, ZINC 2	FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG I;	TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX	(IKANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION	TRANSCRIPTION INITIATION,	INITIATOR ELEMENT, YY1, ZINC 2	RECOGNITION, 3 COMPLEX	(TRANSCRIPTION	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-YANG 1;	TRANSCRIPTION INITIATION,	FINGER PROTEIN DNA-PROTEIN	RECOGNITION, 3 COMPLEX	(TRANSCRIPTION	COMPLEX (TRANSCRIPTION
Coumpound	YY J; CHAIN: C; ADENO- ASSOCIATED VIRUS PS INTIATOR ELEMENT DNA; CHAIN: A, B;		YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS PS	INITIATOR ELEMENT DNA; CHAIN: A, B;			YY1; CHAIN: C; ADENO-	INITIATOR ELEMENT DNA;	CHAIN: A, B;			YY1; CHAIN; C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;			YY1; CHAIN: C; ADENO-
SEQFOL D score																		
PMF	1.00		1.00				1.00					1.00						1.00
Verify score	0.13		0.02				0.21					0.36						0.03
Psi Blast	4.5e-43		1.6e-32				1.5e-46					4.8e-34						1.5e-50
END	303		303				329					359						443
STAR T AA	199		202				223					258						332
CHAI N ID	D D		o o				ပ					0						S
PDB CI	Iubd		pqnI				pqnI				_	Inpq		_				lubd
SEQ NO:	1772		1772				1772					1772		_				1772

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PDB annotation	REGULATIONDNA) YING-YANG I; TRANSCRPTION INITIATION, INITIATOR ELEMENT, YIL ZINC2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRITION)	COMPLEX (TRANSCRIPTION REGILATION/DNA) YING-YANG I; TRANSCRIPTON INITIATION, INITIATON, INITIATON, ENGREEN, TYI, ZINC 2 PINGRE PROTEIN, DAN, PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION)	COMPLEX (TRANSCRIPTION) REGULATION/DNA) YING-YANG I; TRANSCRIPTON INITIATION, INITIATON, ENGREEN REJUSTA, YYI, ZINC 2 FINGER PROTEIN, DIA, PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION)	COMPLEX (TRANSCREPTION) REGILATION/DNA) TING-YANG I; TRANSCREPTON INITIATION, INITIATON, INITIATON, ENGREE PROTEIN, DNA, PROTEIN RECOGNITION, 3 COMPLEX (TRANSCREPTION RECOGNITION, 3 COMPLEX REGILATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG I; TRANSCRIPTION INITIATION,
Coumpound	ASSOCIATED VIRUS PS INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHANF. C; ADBNO- SACCATED VIRUS PS NITIATOR ELEMENT DNA; CHAIN: A, B;	YY; CHAIN: C, ADBNO- SASCIATBO VIRUS PS NITIATONE ELEMENT DINI; CHAIN: A, B;	YY; CIAIN: C, ADBNO- SASCIATED VIRUS PS INITIATOR ELEMENT DIA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA;
SEQFOL D score					82.44
PMF		1.00	0.90	1.00	
Verify		0.06	-0.01	0.01	
Psi Blast		6e-52	9e-51	3e-50	96-51
END		472	499	527	528
STAR T AA		360	388	416	420
CHA!		U	Ü	υ	၁
EDB CI		Inbd	Iubd	Inbd	Inbd
SEQ ID NO:		1772	1772	1772	1772

PDB annotation	INITIATOR BLEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATIONIDNA)	COMPLEX (TRANSCRIPTION REGULATIONNON) YING-YANG I; TRANSCRIPTION INITIATION, INITIATION, INITIATION, INITIATION, EINERST PROTEIN, DAA-BROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION), REGULATION(DNA)	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADRI, ZINC FINGER, NMR	COMPLEX (DNA-BINDING PROTEINDINA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)				COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI;
Coumpound	CHAIN: A, B;	VYI; CHANN: C; ADENO. ASSOCIATED VIRUS FOS INITIATOR ELEMENT DNA; CHAIN: A, B;	ADRI; CHAIN: NULL;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;
SEQFOL D score								
PMF		00'1	-0.18	0.13	0.95	00'1	66.0	86.0
Verify		0.11	0.11	-0.10	0.26	0.51	0.21	0.31
Psi Blast		86-35	8e-14	3.2e-29	3e-58	9c-64	1.5e-63	1.5e-67
END		527	193	246	386	417	445	201
STAR T AA		426	139	102	197	278	306	362
CHAI N ID		υ		∢	٧	<	<	٧
PDB ID		Iubd	2adr	2gli	2gli	2gli	2gli	2gli
SEQ No:		1772	1772	1772	1772	1772	1772	1772

PDB annotation	GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI, GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	TRANSCRIPTION REGULATION PROTO-ONCOGENE, NUCLEAR BODIES (PODS), LEUKEMIA, 2 TRANSCRIPTION REGULATION			LIGASE CBL, UBCH7, ZAP-70, E2, UBQUTIN, B3, PHOSPHORYTA/TION, 2 TYROSINE KINASE, UBIQUITINATION, PROTEIN DEGRADATION,	LIGASE CBL, UBCH7, ZAP-70, E2,
Coumpound		ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	TRANSCRIPTION FACTOR PML; CHAIN: NULL;	VIRUS EQUINE HERPES VIRUS- 1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	VIRUS EQUINE HERPES VIRUS- 1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	SIGNAL TRANSDUCTION PROTEIN CBL, CHARI: A; ZAP- 70 PEPTIDE, CHARI: B; UBIQUITIN-CONUGATING BENZYME E12-18 KDA UBCH7; CHARI: C;	SIGNAL TRANSDUCTION
SEQFOL D score		88.77							
PMF			0.84	00.1	0.07	0.52	0.39	0.41	0.21
Verify			-0.07	0.24	-0.87	-0.50	-0.28	0.41	-0.34
Psi Blast		1.50-67	1.5e-49	1.6e-34	4.8e-06	1.3e-11	3.2e-06	1.26-12	3.2e-06
END		501	524	529	59	59	63	69	59
STAR T AA		362	390	398	10	=	51	4	15
CHAI		¥	Ą	٧				∀	Ą
808 ED		2gli	2gli	2gli	1bor	Ichc	Iche	1fbv	Ifbv
SEQ EQ Si Di Si		1772	1772	1772	1774	1774	1774	1774	1774

PDB annotation	ZAP- UBIQUITIN, E3, PHOSPHORYLATION, 2 TYROSINE XINASE, UBIQUITINATION, PROTEIN DEGRADATION,	ZINC-BINDING PROTEIN ZINC- BINDING PROTEIN, XNF7, BBOX, DEVELOPMENT, 3 MID-BLASTULA- TRANSITION	METAL BINDING PROTEIN RING HOGER PROTEIN MATI; RING FINGER (C3HC4)	T	DMA-BINDING PROTEIN VIDJA RECOMBINATION ACTIVATING PROTEIN I; RAGI, VIOJA RECOMBINATION, ANTEODY, MAD, RING FINGER, 2 ZINC BINGUCLEAR CLUSTER, ZINC FINGER, DIAA-BINDING PROTEIN	DIVA-BINIDING PROTEIN VIDJ RECOMBINATION ACTIVATING RECOMBINATION, ANTIBODY, MAD, RING BINGER, 2 ZINC BINGCLEAR CLOSTER, ZINC FINGRE, DIVA-BINDING PROTEIN	A, STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION 2.2
Coumpound	PROTEIN CBL; CHAIN: A; ZAP- 70 PEPTIDE, CHAIN: B; UB!QUITIN-CONJUGATING ENZYME B12-18 KDA UBCH7; CHAIN: C;	NUCLEAR FACTOR XNF7; CHAIN: NULL;	CDK-ACTIVATING KINASE ASSEMBLY FACTOR MATI; CHAIN: A;	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	RAGI; CHAIN: NULL;	RAĞI; CHAIN: NULL;	ALPHA SPECTRIN; CHAIN: A, B, C;
SEQFOL D score				54.69			
PMF		0.36	0.74		0.84	0.01	0.19
Verify		-0.23	0.21		-0.03	-0.19	-0.07
Psi Blast		1.5e-13	4.5e-14	30-06	4.5e-20	6.4e-14	4.5e-07
END		128	70	304	001	601	414
STAR T AA		8	11	9	=	6	248
CHAI N ID		,	<	¥			<
PDB		lfre	1g25	Iqua	lmd	Irmd	Icun
SEQ No. 19		1774	1774	1774	1774	1774	1775

				_		_	_			
PDB annotation	STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2.2 TANDEM 3-HELIX COLLED-COLLS, STRUCTURAL PROTEIN	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELLX BUNDLE				TRANSCRIPTION HELIX-BUNDLE	TRANSCRIPTION TRANSCRIPTION, RNA POLYMERASE II SUBUNIT, RPB9, ZN RIBBON, 2 HYPERTHERMOPHILIC, BXTREMOPHILE		
Compound		ALPHA SPECTRIN; CHAIN: A, B, C;	SYNTAXIN-14; CHAIN: A, B, C;		VIRUS EQUINE HERPES VIRUS- 1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4		TRANSCRIPTION BLONGATION FACTOR S-II; CHAIN: A;	RNA POLYMERASE II; CHAIN: NULL;	TRANSCRIPTION REGULATION TRANSCRIPTIONAL BLONGATION FACTOR SII (TFIIS, NUCLEIC-ACID ITFI 3 BINDING DOMAIN) (NMR, 12 STRUCTURES) ITFI 4	TRANSCRIPTION REGULATION TRANSCRIPTIONAL ELONGATION FACTOR SII
SEQFOL D score										
PMF		-0.13	-0.12		0.18		0.52	0.51	00.1	0.75
Verify		0.34	0.10		0.21		-0.14	-0.51	0.16	-0.07
Psi Blast		96-10	4.5e-09		0.0006		4.5e-06	0.00045	1.6e-10	4.5e-11
END AA		93	124		553		78	343	345	343
STAR T AA		-	6		516		_	291	286	287
CHAI N ID		₹	A				<			
FDB ID		1cun	lez3		1chc		1eo0	19ур	Ħ	JHĘ
SEQ No.		1776	1776		1777		1780	1780	1780	1780

		 	_																_							
PDB annotation		SIGNAL TRANSDUCTION SRC	TRANSPICATION STIRLE	EPS8, PROLINE RICH PEPTIDE	TRANSFERASE IL-2-INDUCIBLE T-	PEGITI ATORY INTRAMOLECTII AR	COMPLEX, KINASE	KINASE KINASE, SH3 DOMAIN,	TRANSFERASE,	PHOSPHOTRANSFERASE, 2 PROTO-	UNCOGENE, MULTIPLE DOMAIN,	COMPLEX	(TRANSFERASE/PEPTIDE)	COMPLEX	(TRANSFERASE/PEPTIDE), SIGNAL	TRANSDUCTION, 2 SH3 DOMAIN	TRANSFERASE TYROSINE-PROTEIN	KINASE, TRANSFERASE, SIGNAL TRANSDUCTION, 2 SH3	SIGNALING	PROTEIN/TRANSFERASE NAK;	COMPLEX, SIGNAL	TRANSDUCTION,	PHOSPHOTYROSINE BINDING 2	DOMAIN (PTB), ASYMMETRIC CELL	COMPLEX (SH3 DOMAINVIBAT	ENHANCER) SRC-HOMOLOGY 3
Coumpound	(TFIIS, NUCLEIC-ACID 1TFI 3 BINDING DOMAIN) (NMR, 12 STRUCTURES) 1TFI 4	EPS8; CHAIN: A, B;			ITK; CHAIN: NULL;			ABL TYROSINE KINASE;	CHAIN: NULL;			ABL TYROSINE KINASE:	CHAIN: A, C, E, G; PEPTIDE P41;	CHAIN: B, D, F, H;			HEMOPOIETIC CELL KINASE;	CHAIN: A, B, C, D, E, F;	NUMB PROTEIN; CHAIN: A;	NUMB ASSOCIATE KINASE;	CHAIN: B;				FVN TVROSINE KINASE.	CHAIN: A, C, HIV-1 NEF
SEQFOL D score																										
PMF		0.01			0.82			0.92				0.84					00.1		0.63						1 00	3:
Verify		-0.85			06.0			-0.29				-0.27					-0.27		-0.04						51.0	3
Psi Blast		1.5e-14			3e-14			1.2e-11				16-17					4.5e-12		0.003						11.09	
END		210			202			208				208					208		148						202	3
STAR T AA		458			436			459				459					429		84						450	3
CHAI		٧										V					~		V						A	
PDB		laoj			lawj			lawo				16bz		_			lpg1		1ddm			_	_		Ĥe.	
SEQ B) Sign		1781			1781	_		1781				1781					1781		1781						1781	

PDB annotation	DOMAIN, COMERY KIBB DOMAINVINAL ENERANCER, PROTO-ONCOGENE, 2 TRANSTERASE, TROSINE- PROTEN KINASE, PROSTRIVATON, CIP-BINDING, MYRISTYLATION, CIP-BINDING, THE BINDING, STEP BOOKANI, STE DOMAIN, PRI HEILX, PXXP MOTIF	TRANSFERASE PROTO-ONCOGENE TYROSHUE KINASE; PROTO- ONCOGENE, TRANSFERASE, TYROSHUE-ROTHER KINASE, TYROSHUE-RATION, KINASE, MYRISTYLATION, SH3 DOMAIN, 3 COMPILEX COMPILEX	COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE) COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE), SH3 DOMAIN		COMPLEX (KINASE/PEPTIDE)
Coumpound	PROTEIN: CHAIN: B, D;	PHOSPHOTRANSFERASE FYN; CHAIN: A; 3BP-2; CHAIN: B;	GRB2, CHAIN: A; SOS-1; CHAIN: B;	SIGNAL TRANSDUCTION PROTEIN GROWTH FACTOR RECEPTOR-BOUND PROTEIN GREAT AFTERMINAL I GRBR 3 SH3 DOMAND, COMPLEXED WITH SOSA PEPTIDE I GBR 4 (NNR, 29 STRUCTURES) I GBR 5	P56==LCK== TYROSINE KINASE; ILCK 7 CHAIN: A; ILCK 8 TAIL PHOSPHOPEPTIDE TEGQ(PHOSPHO)YQPQPA;
SEQFOL D seore					
PMF		1.00	0.84	0.74	10:0
Verify		0.07	-0.33	-0.35	-0.41
Psi Blast		16-11	1.46-12	30-13	4.8e-19
END		208	208	510	581
STAR T AA		457	454	446	456
CHAI		⋖	∢	⋖	∢
an and		lfyn	Igbq	1gbr	llek
SEQ NO.		1781	1781	1781	1781

PDB annotation		COMPLEX (TRANSFERASE/PEPTIDE) SRC, SH3 DOMANN, LIGANDS, NON-PEPTIDE ELEMENTS, 2 COMPLEX (TRANSFERASE/PETIDE)	CIRCULAR PERMUTANT PWT; CIRCULAR PERMUTANT, SH3 DOMAIN, CYTOSKELETON	TYROSINE KINASE TYROSINE KINASE-INHIBITOR COMPLEX, DOWN-REGULATED KINASE, 2 ORDERED ACTIVATION I OOP	CYTOSKELETON CYTOSKELETON, MEMBRANE, SH3 DOMAIN	TYROSINE-PROTEIN KINASE BRUTONS TYROSINE KINASE, B CELL PROGENITOR KINASE, ITRANSERASE, TYROSINE- PROTEIN KINASE, PROTEIN KINASE, PROSTINI KINASE, DOMAIN		CBLLOYCLEGENERECULATION COMPLEX SIGNAL. TRANSDUCTION, PROSPHOTYROSINES BINDING 2 DOMARN (FTB), ASYMETR IC CELL DIVISION, CELL CYCLEGENE 3 REGILI ATION	TRANSFERASE HCK: SH3, PROTEIN
Coumpound	ILCK 14 CHAIN: B; ILCK 15	C-SRC; CHAIN: C; NLI (MN7- MN2-MNI-PLPPLP); CHAIN: N;	ALPHA SPECTRIN; CHAIN: NULL;	HAEMATOPOETIC CELL KINASE (HCK); CHAIN: A;	ALPHA II SPECTRIN; CHAIN: A;	TYROSINE-PROTEIN KINASE BTK; CHAIN: A;	PHOSPHOTRANSFERASE FYN PROTO-ONCOGENE TYROSINE KINASE (E.C.2.7.1.112) 1SHF 3 (SH3 DOMAIN) 1SHF 4	NUMB PROTEIN; CHAIN: A; GPPY PEPTIDE; CHAIN: B;	HEMATOPOIETIC CELL
SEQFOL D score									
PMF		0.1	1.00	0.15	1.00	0.81	00'1	0.64	1.00
Verify		0.18	0.21	-0.31	0.20	-0.05	-0.64	0.25	0.46
Psi Blast		3e-11	3e-10	3.2e-18	1.5e-10	3e-12	7,5e-11	36-12	7.5e-12
END		507	208	581	208	208	208	153	208
STAR T AA		459	457	456	457	455	459 ·	27	455
CHAI N ID		0		V	⋖	4	Ą	A	
EDB ID		1nlo	lpwt	Jobl	Iqkw	Iqly	Ishf	2nmb	4hck
SEQ NO.		1781	1781	1781	1781	1781	1781	1781	1781

PDB annotation	TYROSINE KINASE, SIGNAL TRANSDUCTION, 2 TRANSFERASE	COMPLEX (TRANSCRIPTION PACTORIONA) TRANSCRIPTION PACTOR, PROTEIN-DINA COMPLEX, CYTOKINE 2 ACTIVATION, COMPLEX (TRANSCRIPTION PACTORIONA)		STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HALCAL LINKER REGION, 2 2 HANDEM 3-HELIX COLED-COLES, STRUCTURAL PROTEIN	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P354, THREE HELIX BUNDLE	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE
Соимроила	KINASB; CHAIN: NULL;	STAT3B; CHAIN: 4; 18-MER DESOXYOLIGONUCLEOTIDE; CHAIN: B;	APOLIPOPROTEIN E; CHAIN: A;	ALPHA SPBCTRIN; CHAIN: A, B, C;	SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	SYNTAXIN-1A; CHAIN: A, B, C,	SYNTAXIN-1A; CHAIN: A, B, C;	SYNTAXIN-1A; CHAIN: A, B, C,
SEQFOL D score								
PMF		0.04	0.04	-0.06	0.30	0.28	0.00	0.18
Verify	1000	0.07	0.20	0.04	-0.22	0.11	-0.41	-0.04
Psi Blast		1.1e-07	1.6e-05	36-13	7.5e-19	4.5e-07	1.5e-08	1e-09
END		861	126	259	298	260	298	394
STAR T AA		36	6	24	78	118	138	246
CHAI N ID		<	<	∢	æ	Y Y	∢	٧
eg a		lbg1	1bz4	lcun	1dn1	lez3	lez3	lez3
SEQ NO.		1782	1782	1782	1782	1782	1782	1782

PDB annotation	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX	MEMBRANE PROTEIN FOUR HELIX BUNDLE, ALPHA HELIX	DNA-BINDING HMGA DNA- BINDING HMG-BOX DOMAIN A OF RAT HMGI; IAAB 8 HMG-BOX IAAB 20	SIGNALING PROTEIN GUANINE NUCLEOTIDE BINDING RECIEN 1; GBP, GTP HYDROLYSIS, GDP, GAVE NUTERFER ON INDUCED, DYNAMIN NERFER ON INDUCED, DYNAMIN STREATH, LARGE GTP ASE FAMILY, SIGNALING PROTEIN	SIGNALING PROTEIN GBP, GTP HYDROLYSUS, GDP, GMP, INTERERON INDUCED, DYNAMIN 2 RELATED, LARGE GTPASE FAMILY, GMPPNR, GPPNRP.	SERINE/THREONINE PROTEIN KINASE TRAANSERASAS, SERINE/THREONINE-PROTEIN KINASE, 2 PROTO-ONCOGENE, ZINC, ATT-ENDING, PHORBOL- ESTER BINDING		SIGNALLING PROTEIN TYPE I RECEPTOR, STNFRI; 1NCF 8
Coumpound	SSOI PROTEIN; CHAIN: A;	SSOI PROTEIN; CHAIN: A;	HIGH MOBILITY GROUP PROTEIN; 1AAB 5 CHAIN: NULL; 1AAB 6	INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN I; CHAIN: A;	INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1; CHAIN: A;	RAF-1; CHAIN: NULL;	DNA-BINDING HIGH MOBILITY GROUP PROTEIN FRAGMENT-B (HMGB) (DNA- BINDING IHMG 3 HMG-BOX DOMALN B OF RAT HMGI) DOMALI STRUCTURE) HMG4	TUMOR NECROSIS FACTOR RECEPTOR; INCF 4 CHAIN: A,
SEQFOL D score								
PMF	0.04	0.03	0.03	0.19	0.04	0.03	0.00	0.12
Verify score	-0.09	-0.28	-0.24	0.02	0.02	-0.40	-0.29	0.02
Psi Blast	7.5e-07	16-11	0.00012	4.5e-05	0.00015	0.003	0.0045	900.0
END	485	280	763	2333	2333	&	753	141
STAR T AA	283	65	716	2237	2237	89	716	17
CHAI	¥	∢		∢	¥			A
PDB	1ffo	1ff0	laab	1dg3	If5n	Ifaq	Ihme	lncf
SEQ EQ	1782	1782	1783	1783	1783	1783	1783	1783

	,					_		_		
PDB annotation	BINDING PROTEIN, CYTOKINE INCF 19	PHOSPHOTRANSFERASE	CALCIUM-BINDING PROTEIN RAT BRAIN PKC-G; CALCIUM-BINDING PROTEIN, PROTEIN KINASE C, PKC, TRANSFERASE	CALCIUM-BINDING PROTEIN RAT BEAIN PKC-G; CALCIUM-BINDING PROTEIN, PROTEIN KINASE C, PKC, TRANSFERASE	GENE REGULATION/DNA LEF-I HAGG, LEFH, HAGG, FCR-A, TRANSCRIPTION FACTOR, DNA BINDING, DNA 2 BENDING, COMPLEX (HMG DOMAIN/DNA), GENE REGULATION/DNA		CALCIUM-BINDING PROTEIN RAT BRAIN PKC-G; CALCIUM-BINDING PROTEIN, PROTEIN KINASE C, PKC, TRANSFERASE		COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	
Coumpound	B; INCF 5	PROTEIN KINASE C DELTA TYPE; 1PTQ 4	PROTEIN KINASE C, GAMMA TYPE; CHAIN: NULL;	PROTEIN KINASE C, GAMMA TYPE; CHAIN: NULL;	LYMPHOID ENHANCER- BINDING FACTOR; CHAIN: A; DINA (5'-CHAIN: B; DNA (5'- CHAIN: C;		PROTEIN KINASE C, GAMMA TYPE; CHAIN: NULL;		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE: CHAIN: B. C.	DNA-BINDING PROTEIN HUMAN ENFANCER-BINDING PROTEIN MBP-1 MUTANT WITH CYS 11 1BBO 3 KREPLACED BY ABU (C1ABU) (NMR, 60 STR UCTURES) 1BBO
SEQFOL D score										
PMF		0.23	0.31	0.41	0.31		0.01		0.45	-0.13
Verify		0.02	-0.09	-0.35	-0.13		-0.65		-0.30	0.07
Psi Blast		0.003	0.00075	9:00:0	7.5e-05		0.0000		3.2e-26	3.2e-12
END		20	50	66	763		137		130	232
STAR T AA		21	21	69	716		100		62	178
CHAI N ID					4				∀	
PDB ID		lptq	Ith	1tbn	2lef		Itbn			1bbo
SEQ B B Ö		1783	1783	1783	1783		1784			1785

PDB annotation			COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADR1, ZINC FINGER, NMR	COMPLEX TRANSGEDTION REGULATION/DNA) GABPALPHA; GABBETAL; COMPLEX (TRANSCRETION) REGULATION/DNA) DNA-BINDING, REGULATION/DNA), DNA-BINDING, ANYKRIN REPARTEN
Coumpound	4	DNA-BINDING PROTEIN HUMANI BRHANCER-BINDING PROTEIN MBP-1 MUTANT WITH CYS 11 1BBO 3 REPLACED BY ABU (CILABU) (NMR, 60 STRUCTURES) 1BBO	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	ADRI; CHAIN: NULL;	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;
SEQFOL D seore							
PMF		0.04	0.04	0.04	0.05	06:0	0.52
Verify score		-0.88	-0.42	-0.19	-0.23	-0.01	-0.23
Psi Blast		1.6e-12	1.6e-42	4.8e-41	3.2e-12	4.8c-18	8e-34
END		113	98	114	114	117	157
STAR T AA		2	15	43	87	62	81
CHAI N ID			o	၁	5		я
PDB ID		1660	lmey	1mey	Ішеу	2adr	Iawc
SEQ NO:		1785	1785	1785	1785	1785	

PDB annotation	TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION REGULATIONIDNA) OABA ALPHA; GABPBETAI; COMPLEX (TRANSCRIPTION REGULATIONIDNA, DIAV-BRUDING, 2 NUCLEAR PROTEIN, ETS DOMAIN,	ANK TRIN REPEATS, TRANSCRIPTION 3 FACTOR TÜMÖR SUPPRESSOR TÜMÖR SUPPRESSOR, CDK4/6 INHIBITOR,	COMPLEX (KINASE/ANTI- ONCOGENE) CDK6: P16INK4A.	MTSI; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT	KINASE INHIBITORY 2 PROTEIN,	TUMOR SUPPRESSOR, 3 MTS1,	COMPLEX (KINASE/ANTI- ONCOGENE) HEADER	-	_	KINASE, CELL CYCLE 2 CONTROL,	(INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR	-	ALPHA/BETA, COMPLEX	(INHIBITOR PROTEIN/KINASE)	HORMONE/GROWTH FACTOR P18-
Coumpound		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	PI9INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	CYCLIN-DEPENDENT KINASE 6: CHAIN: A: MULTIPLE	TUMOR SUPPRESSOR; CHAIN: B;				CYCLIN-DEPENDENT KINASE	9; CEMIN: A; r PHINN4D; CEMIN: B;			CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19TNK4D; CHAIN:	B;			CYCLIN-DEPENDENT KINASE
SEQFOL D score																	
PMF		0.29	61.0	0.04					0.00				0.37				0.15
Verify		-0.09	10:0-	0.14					-0.17				0.01				-0.12
Psi Blast		4.8e-29	80-27	6.4e-17					6.4e-26				1.3e-23				6.4e-25
END		125	160	999					160				183				130
STAR T AA		e	21	443					21				ος 20				-
CHAI N ID		В		В					ш				en en				A
EDB ED		Iawc	1bd8	1bi7					Nd1				1blx			1	lbug
SEQ ID NO:		1788	1788	1788					1788				1788			\neg	1788

						, -			,
PDB annotation	INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR	SIGNALING PROTEIN HELIX-TURN- HELIX, ANKYRIN REPEAT	CELL CYCLE INHIBITOR P18- INK4C(INK6), CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR	CELL CYCLE INHIBITOR P18- INK4C(INK6), CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANK YRIN REPEAT, 2 CDK 4/6 INHIBITOR.	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT	SIGNALING PROTEIN RUBI, UBIQUITIN-LIKE PROTEIN, ARABIDOPSIS, SIGNALING PROTEIN	DE NOVO PROTEIN PROTEIN DESIGN, HYDROPHOBIC CORE, PACKING, ROTAMERS, ROC, 2 UBIQUITN, DE NOVO PROTEIN, UBIOLITIN	SIGNALING PROTEIN NEDDS; NEDDS, NEDD-8, UBIQUITIN-LIKE, PROTEOLYSIS, SIGNALING 2 PROTEIN	
Coumpound	6 INHIBITOR; CHAIN: A;	CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	MYOTROPHIN; CHAIN: NULL	UBIQUITIN-LIKE PROTEIN 7, RUBI; CHAIN: A;	ID8 UBIQUITIN; CHAIN: A;	UBIQUITIN-LIKE PROTEIN NEDD8; CHAIN: A, B, C, D;	UBIQUITIN TETRAÜBIQUITIN ITBE 3
SEQFOL D seore									
PMF		90.0	0.10	0.37	0.01	0.92	0.76	0.75	0.94
Verify		0.14	-0.12	0.01	0.14	0.17	0.02	0.22	0.48
Psi Blast		1.6e-17	1.3e-25	3.2c-24	1.6e-20	1.4e-20	1.6e-27	6.4e-20	3.2e-27
END		267	191	129	127	194	196	195	193
STAR		443	81	_	61	124	124	124	124
CHAI N ID		A	∢	¥		¥	∢	4	В
an T		s6pt	911	1116	1myo	1540	le3t	lndd	1tbe
S e S		1788	1788	1788	1788	1791	1621	1621	1621

PDB annotation		UBIQUITIN UBIQUITIN, DESIGNED CORE MUTANT	TRANSCRIPTION TUMOR SUPPRESSOR, CANCER, UBIQUITIN, BETA SANDWICH, 2 TRANSCRIPTION, TRANSCRIPTIONAL ELONGATION	MATRIX PROTEIN M-PMV MA MATRIX PROTEIN, CORE PROTEIN, POI VDROTEIN MYPISTYI ATION	MATRIX PROTEIN M-BAV MA MATRIX PROTEIN, CORE PROTEIN, POLYPROTEIN, MYRISTYLATION	ENDOCYTOSIS/EXOCYTOSIS NSECI, PROTEIN-PROTEIN COMPLEX, MULTI-SUBLINIT	ENDOCYTOSIS/EXOCYTOSIS NSECI; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT	MUSCLE PROTEIN CTNG; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCHIM PINDING	MUSCLE PROTEIN CTNC; CARDIAC, MUSCLE PROTEIN, REGULATORY, CALCIUM BINDING	CALCIUM-BINDING PROTEIN CALMODULIN CERIUM TRIC- DOMAIN, RESIDUES 1 - 75; CERIUM-
Coumpound	CHROMOSOMAL PROTEIN UBIQUITIN 1UBI 3	UBIQUITIN CORE MUTANT ID7; CHAIN: A;	ELONGIN B; CHAIN: A, D, G, J; ELONGIN C; CHAIN: B, E, H, K; VHL; CHAIN: C, F, I, L;	M-PMV MATRIX PROTEIN; CHAIN: NULL;	M-PMV MATRIX PROTEIN; CHAIN: NULL;	SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CHAIN: B;	TROPONIN C; CHAIN: NULL;	TROPONIN C; CHAIN: NULL;	CALMODULIN; CHAIN: NULL;
SEQFOL D score					69.49			57.92		
PMF	99'0	0.55	0.15	0.64		0.00	0.00		0.25	-0.01
Verify	0.19	0.39	-0.54	-0.22		-0.04	-0.04		0.30	0.12
Psi Blast	4.8e-29	3,2e-28	6.4e-0.5	3,2e-36	3,2e-36	0.0075	0.0075	6.40-36	6.4e-36	4.8c-16
END	196	196	181	92	92	227	235	382	379	309
STAR	124	124	124	-	_	157	165	225	241	241
CHAI N ID		٧	¥			В	В			
PDB ID	1ubi	1nd7	lvcb	1bax	1bax	Idn1	1dn1	laj4	1854	1ak8
SEQ NO.	1621	1791	1791	1792	1792	1794	1795	1799	1799	1799

		HON,			LATE	LATE	f- LATE			
otation	LOADED, CALCIUM-BINDING PROTEIN	CALCIUM-BINDING CNTINC; CALCIUM-BINDING, REGULATION, TROPONIN C, CARDIAC MUSCLE 2, CONTRACTION	HYDROLASE CALCINBURIN; HYDROLASE, PHOSPHATASE, IMMUNOSUPPRESSION	HYDROLASE CALCINEURIN; HYDROLASE, PHOSPHATASE, IMMUNOSUPPRESSION	CALCIUM-BINDING CALCIUM- BINDING, MYRISTOYLATION, NEURONAL SPECIFIC GUANYLATE 2 CYCLASE ACTIVATOR	CALCIUM-BINDING CALCIUM- BINDING, MYRISTOYLATION, NEURONAL SPECIFIC GUANYLATE 2 CYCLASE ACTIVATOR	CALCIUM-BINDING CALCIUM- BINDING, MYRISTOYLATION, NEURONAL SPECIFIC GUANYLATE 2 CYCLASE ACTIVATOR			
PDB annotation	CALCIUM	-BINDING -BINDING V C, CARD	TYDROLASE CALCINET TYDROLASE, PHOSPHA MMUNOSUPPRESSION	HYDROLASE CALCINEURIN; HYDROLASE, PHOSPHATASE IMMUNOSUPPRESSION	-BINDING MYRISTO AL SPECIF E ACTIVA	CALCIUM-BINDING CAL BINDING, MYRISTOYLA NEURONAL SPECIFIC GL	CALCIUM-BINDING CAL BINDING, MYRISTOYLA NEURONAL SPECIFIC GI 2 CYCLASE ACTIVATOR			
	LOADED, PROTEIN	CALCIUM-BINDING CNTNC; CALCIUM-BINDING, REGUIL, TROPONIN C, CARDIAC MUS	HYDROLASE CALCINEURIN; HYDROLASE, PHOSPHATASI IMMUNOSUPPRESSION	HYDROL/ HYDROL/ IMMUNOS	CALCIUM-BINDING CAL BINDING, MYRISTOYLA' NEURONAL SPECIFIC GU 2 CYCLASE ACTIVATOR	CALCIUM BINDING, NEURON/ 2 CYCLAS	CALCIUM BINDING, NEURONA 2 CYCLAS			
		Ú	AIN: A,	AIN: A,				OTEIN EXED INDING INDING	OTEIN BRATE)	
Coumpound		ROPONIN;	SE 2B; CH,	SONINE SE 2B; CH,	IN DELTA	IN DELTA	IN DELTA	NDING PR N COMPLI NDULIN-B ICDM 3 N-DEPENT ASE II ICI	NDING PR N (VERTE	
Ö		CARDIAC N-TROPONIN C; CHAIN: NULL;	SERINE/THREONINE PHOSPHATASE 2B; CHAIN: A, B:	SERINE/THREONINE PHOSPHATASE 2B; CHAIN: A, B:	NEUROCALCIN DELTA; CHAIN: A, B;	NEUROCALCIN DELTA; CHAIN: A, B;	NEUROCALCIN DELTA; CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALMODULIN COMPLEXED WITH CALMODULIN-BINDING DOMAIN OF ICDM 3 CALMODULIN-DEPENDENT CALMODULIN-DEPENDENT	CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) ICLL 3	
-	_	35	S E 8	E E E	₽ 5	夏哥	見ぎ	\$58¥85¥	335	
SEQFOL D score			69.73				59.92			
PMF		-0.01		89.0	0.19	0.83		0.18	0.21	
Verify		0.50		0.46	-0.02	0.64		0.25	0.05	1
Psi Blast		1.4c-12	4.8e-42	4.8e-42	3.2e-11	6.4e-36	6.4e-36	3.26-42	3.2e-47	
END		314	391	378	345	385	390	378	378	000
STAR T AA		241	233	240	202	224	224	241	241	.,,
CHAI N ID			В	B	<	∢	×.	∢		
EDB EDB		lap4	1aui	laui	16Jf	1bJf	lbjf	1cdm	Icil	-
SEQ NO ID		1799	1799	1799	1799	1799	1799	6621	1799	1200

PDB annotation		CALCIUM-BINDING PROTEIN CALMODULIN APO TR2C-DOMAIN; ICMF 9	CALCIUM-BINDING PROTEIN CALMODULIN APO TR2C-DOMAIN; ICMF 9	BLOOD CLOTTING HELICAL, EF- HAND, BLOOD CLOTTING	STRUCTURAL PROTEIN HELLX- TURN-HELIX	STRUCTURAL PROTEIN HELIX- TURN-HELIX	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER	TRANSPORT PROTEIN CALCIUM BINDING, EF HAND, FOUR-HELIX BUNDLE	TRANSPORT PROTEIN CALCIUM BINDING, EF HAND, FOUR-HELIX BUNDLE	CONTRACTILE PROTEIN TROPONIN C-TROPONIN I INTERACTION, CARDIAC, MUSCLE PROTEIN, 2 CALCIUM BINDING PROTEIN	CONTRACTILE PROTEIN TROPONIN C-TROPONIN INTERACTION, CARDIAC, MUSCLE PROTEIN, 2 CALCITM BINDING PROTEIN	METAL BINDING PROTEIN YEAST FREOUENIN EP-HAND, CALCIUM	LYASE GCAP-2; EF-HAND, CALCIUM-BINDING PROTEIN,
Coumpound	CALMODULIN (VERTEBRATE) 1CLL 3	CALMODULIN (VERTEBRATE); ICMF 6 CHAIN: NULL; ICMF 7	CALMODULIN (VERTEBRATE); ICMF 6 CHAIN: NULL; ICMF 7	APO CIB; CHAIN: A	CARDIAC TROPONIN C; CHAIN: A;	CARDIAC TROPONIN C; CHAIN: A;	CALMODULIN; CHAIN: A;	CALMODULIN; CHAIN; A;	CALMODULIN; CHAIN: A;	TROPONIN C; CHAIN: A;	TROPONIN C; CHAIN: A;	CALCIUM-BINDING PROTEIN NCS-1; CHAIN: A;	GUANYLATE CYCLASE ACTIVATING PROTEIN 2;
SEQFOL D score													
PMF		0.13	-0.06	09:0	0.07	69.0	0.12	0.60	0.16	0.21	0.18	0.03	0.99
Verify		0.73	0.43	0.01	90.0	0.16	0.13	0.40	0.44	0.25	0.10	0.18	0.46
Psi Blast		4.8e-11	1.6e-25	3.2e-20	1.4e-12	8e-36	1.3e-44	80-11	3.2e-24	9.6e-10	1.3e-19	3.2e-15	1.6e-29
END		309	378	388	306	379	378	309	378	306	379	341	392
STAR		242	310	241	183	241	241	247	316	238	313	221	241
CHAI N ID				₹	٧	¥	¥	٧	Ą	¥	Ą	Ą	Ą
PDB ID		lcmf	lcmf	1dgv	Idtl	Idi	lexr	141	1731	1fi5	1fi5	Ifpw	1jba
SEQ ID NO:		1799	1799	1799	1799	1799	1799	1799	1799	1799	1799	1799	1799

PDB annotation	GUANYLYL CYCLASE 2 REGULATION	CALCIUM-REGULATED MUSCLE CONTRACTION MUSCLE CONTRACTION, CALCIUM-	BINDING, TROPONIN, E-F HAND, 2 OPEN CONFORMATION	REGULATORY DOMAIN, CALCIUM- REGULATED 3 MUSCLE CONTRACTION	CALCIUM-REGULATED MUSCLE	CONTRACTION MUSCLE	BINDING, TROPONIN, E-F HAND, 2	OPEN CONFORMATION REGULATORY DOMAIN CALCITIM-	REGULATED 3 MUSCLE	CONTRACTION	CALCIUM-BINDING PROTEIN EF: HAND 1TNX 14	CALCIUM-BINDING PROTEIN EF-	HAIND LINA 14									
Coumpound	CHAIN: A;	TROPONIN C; CHAIN: NULL;			TROPONIN C; CHAIN: NULL;						TROPONIN C; 1TNX 4 CHAIN: NULL; 1TNX 5	TROPONIN C; ITNX 4 CHAIN:	CONTRA COM P. CARGOTTA	PROTEIN TROPONIN C 1TOP 3	CONTRACTILE SYSTEM	PROTEIN TROPONIN C 1TOP 3	CALCIUM BINDING PROTEIN	CALMODULIN (/TR-2-C\$	PRAGMENI COMPRISING	THE INTACT MOLECULE) ITEC	4	CALCIUM BINDING PROTEIN CALMODULIN (/TR=2=C\$
SEQFOL D score					63.35						69.19		10.00	10.40								
PMF		0.48								-		0.05			0.41		-0.05					-0.09
Verify score		0.10										-0.22			0.02		0.28					0.03
Psi Blast		3.2e-37			3.2e-37						4.8e-36	4.8e-36	20. 30	3.25-36	3.20-38		6.4e-11					1.16-24
END AA		378			379						378	378	200	205	378	100	306					378
STAR T AA		232			233						233	236	200	777	236	9,0	242					314
CHAI N ID																	Α.					A
PDB ED		Itef			Ite					1	XE.	Itnx	1	don	Itop		2				_	Itre
SeQ No De		1799			1799						1799	1799	1200	1133	1799	905	66/1					1799

PDB annotation		CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)	MUSCLE PROTEIN MYOSIN, CALCIUM BINDING PROTEIN, MUSCLE PROTEIN	CALCIUM-BINDING PROTEIN CTINC; CARDIAC, MUSCLE, REGULATORY, CALCIUM-BINDING PROTEIN	CALCTUM-BINDING PROTEIN CTNC; CARDIAC, MUSCLE, REGULATORY, CALCIUM-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTFIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTFIN
Coumpound	FRAGMENT COMPRISING RESIDUES 78 - 148 ITRC 3 OF THE INTACT MOLECULE) ITRC 4	CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN; CHAIN: A; RS20; CHAIN: B;	SCALLOP MYOSIN; CHAIN: A, B, C;	TROPONIN C; CHAIN: NULT;	TROPONIN C; CHAIN: NULL;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE: CHAIN: B. C:	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE: CHAIN: B. C:
SEQFOL D score			56.76						
PMF		0.07		0.33	0.04	0.13	0.12	0.35	86.0
Verify		-0.21		0.12	0.23	0.36	0.19	0.03	0.03
Psi Blast		1.6e-14	3.2e-46	3.2e-46	1.4e-20	9.6e-10	1.3e-19	1.6e-12	4.8e-19
END AA		309	381	378	382	306	379	210	238
STAR T AA		180	239	241	241	238	313	120	158
CHAI N ID		¥.	Ą	V	U			4	V
FDB TD		lvrk	lvrk	lvrk	1wdc	3cm	3cm	lalh	lalh
SEQ NO:		1799	1799	1799	1799		1799	1801	1801

-	CHAI	-	二	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
en N		TAA	¥4		score	score	D score		
lalh A		214	296	4.5e-37			84.50	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA),
								OLIGONUCLEOTIDE BINDING SITE; CHAIN; B, C;	ZINC FINGER, DNA-BINDING PROTEIN
lalh A		270	377	1.1e-29	0.23	1.00		QGSR ZINC FINGER PEPTIDE;	COMPLEX (ZINC FINGER/DNA)
_								CHAIN: A; DUPLEX	COMPLEX (ZINC FINGER/DNA),
								OLIGONUCLEOTIDE BINDING SITE: CHAIN: B. C.	ZINC FINGER, DNA-BINDING PROTEIN
lalh A	1	270	377	9.6e-22	-0.16	0.41		OGSR ZINC FINGER PEPTIDE:	COMPLEX (ZINC FINGER/DNA)
								CHAIN: A; DUPLEX	COMPLEX (ZINC FINGER/DNA),
_						_		OLIGONUCLEOTIDE BINDING	ZINC FINGER, DNA-BINDING
-								SITE; CHAIN: B, C;	PROTEIN
lalh A		298	404	1.6e-19	0.22	0.57		QGSR ZINC FINGER PEPTIDE;	COMPLEX (ZINC FINGER/DNA)
		_						CHAIN: A; DUPLEX	COMPLEX (ZINC FINGER/DNA),
								OLIGONUCLEOTIDE BINDING	ZINC FINGER, DNA-BINDING
4	- (SITE; CHAIN: B, C;	PROTEIN
lath A		298	454	3e-19	0.11	99.0		QGSR ZINC FINGER PEPTIDE;	COMPLEX (ZINC FINGER/DNA)
_								CHAIN: A; DUPLEX	COMPLEX (ZINC FINGER/DNA),
_								OLIGONUCLEOTIDE BINDING	ZINC FINGER, DNA-BINDING
-	- (SITE; CHAIN: B, C;	PROTEIN
lalh A		353	481	3e-21	0.07	0.78		QGSR ZINC FINGER PEPTIDE;	COMPLEX (ZINC FINGER/DNA)
								CHAIN: A; DUPLEX	COMPLEX (ZINC FINGER/DNA),
								OLIGONUCLEOTIDE BINDING	ZINC FINGER, DNA-BINDING
laih A	Ĺ	382	481	3.2c-26	0.17	0.15		OGSR ZINC FINGER PEPTIDE:	COMPLEX (ZINC FINGER/DNA)
								CHAIN: A; DUPLEX	COMPLEX (ZINC FINGER/DNA).
_								OLIGONUCLEOTIDE BINDING	ZINC FINGER, DNA-BINDING
_	- 1							SITE; CHAIN: B, C;	PROTEIN
lalh A		459	209	8e-30	0.45	1.00		QGSR ZINC FINGER PEPTIDE;	COMPLEX (ZINC FINGER/DNA)
_		_						CHAIN: A; DUPLEX	COMPLEX (ZINC FINGER/DNA),
_		_						OLIGONUCLEOTIDE BINDING	ZINC FINGER, DNA-BINDING
-	- (SITE; CHAIN: B, C;	PROTEIN
lalh A		429	510	96-31	0.54	1.00		QGSR ZINC FINGER PEPTIDE; CHAIN: A: DUPLEX	COMPLEX (ZINC FINGER/DNA)
	1								

SEQ PDB			STAR T AA	END	Psi Blast	Verify	PMF	SEQFOL D score	Coumpound	PDB annotation
1	-								OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	ZINC FINGER, DNA-BINDING PROTEIN
a a	Ialh A	457		537	1.1e-30	-0.09	1.00	-	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLLGONUCLEOTIDE BINDING SITE: CHAIN: B. C.	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTFIN
lalh	ч ч	48	485	565	7.5e-34	0.28	1.00		GGR ZINC FINGER PEPTIDE; QGR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE: CHAIN: B. C.	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
Ē	Imey C	=	611	210	8e-30	0.10	0.36		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
Ē	lmey C	2	157	238	1.4e-37	0.42	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1mey	c c	31	185	266	3.2c-47	0.55	00:1		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
Imey	C c	23	213	294	3.2e-48	0.35	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN: CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
lê l	Imey C	241		322	4.8e-49	0.56	1.00		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX

S a S	EDB ID	CHAI N ID	STAR T AA	END	Psi Blast	Verify	PMF	SEQFOL D score	Coumpound	PDB annotation
										(ZINC FINGER/DNA)
1801	Imey	C	241	323	4.8e-49			101.14	DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
	_								PROTEIN: CHAIN: C. F. G.	INTERACTION, PROTEIN DESIGN 2
									5 116	CRYSTAL STRUCTURE, COMPLEX
										(ZINC FINGER/DNA)
1801	1mey	2	569	377	4.8e-40	-0.06	0.51		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
									CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
		-								CRYSTAL STRUCTURE, COMPLEX
										(ZINC FINGER/DNA)
1801	lmey	ပ	297	453	1.1e-20	10.0	-0.17		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
									CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
		_					_		PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
_										CRYSTAL STRUCTURE, COMPLEX
										(ZINC FINGER/DNA)
1801	lmey	ပ	353	481	1.3e-22	0.42	0.70		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
									CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
										CRYSTAL STRUCTURE, COMPLEX
7										(ZINC FINGER/DNA)
1801	lmey	υ	357	453	8e-41	0.41	0.24		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
									CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
_			_						PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
										CRYSTAL STRUCTURE, COMPLEX
1801	imey	0	381	481	3.2e-45	0.26	0.07		DNA: CHAIN: A. B. D. E.	COMPLEX (ZINC FINGER/DNA) ZINC
									CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
_									PROTEIN; CHAIN: C, F, G,	INTERACTION, PROTEIN DESIGN, 2
									,	CRYSTAL STRUCTURE, COMPLEX
7										(ZINC FINGER/DNA)
1801	lmey	ပ	428	203	1.6e-49	15.0	00.1		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
	_								PROTEIN: CHAIN: C. F. G.	INTERACTION, PROTEIN DESIGN, 2

	_			_				_					_			_		_			_		_	_				
PDB annotation	CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX	CINC FINGER/DNA)	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRISIAL SIRUCIURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) TFIIIA; 5S	GENE; NMR, TFIIIA, PROTEIN, DNA,	TRANSCRIPTION FACTOR, 5S RNA 2	GENE, DNA BINDING PROTEIN,	ZINC FINGER, COMPLEX 3	(TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) COMPLEX	(TRANSCRIPTION	REGULATION/DNA), RNA	POLYMERASE III, 2	TRANSCRIPTION INITIATION, ZINC	FINGER PROTEIN	COMPLEX (TRANSCRIPTION	REGULATION/DNA) COMPLEX	(TRANSCRIPTION	REGULATION/DNA), RNA	POLYMERASE III, 2	TRANSCRIPTION INITIATION, ZINC
Coumpound		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;	DNA: CHAIN: A B D E:	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;		TRANSCRIPTION FACTOR IIIA;	CHAIN: A; 5S RNA GENE;	CHAIN: E, F;						TFIIIA; CHAIN: A, D; 5S	RIBOSOMAL RNA GENE;	CHAIN: B, C, E, F;					TFUIA; CHAIN: A, D; 5S	RIBOSOMAL RNA GENE;	CHAIN: B, C, E, F;			
SEQFOL D score																							114.65					
PMF		66'0		1 00				-0.01								0.22												
Verify score		-0.03		0.25	!			0.23								0.08								_				
Psi Blast		1.6e-49		1.6e-49				6.4e-17								1.4c-22							3e-61					
END AA		537		565				481								247							325					
STAR		456		484				382								112							157					
CHAI N ID		ပ		U				V								۷		_					∀					
PDB ID		Imey		Imev				Em.	_							1£6						+	1 <u>1</u> 2					
SEQ NO.		1801		1801				1801								1081							1801					

PDB annotation	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMEKASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRETION REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRETION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATIONDA), COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA POLYMERASE II, 2 TRANSCRIPTION INITIATION, ZINC PRICER PROFEN	COMPLEX (TRANSCRIPTION REGULATIONIDADA) COMPLEX (TRANSCRIPTION REGULATIONIDADA), RNA REGULATIONIDADA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC
Coumpound	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL INA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL INA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;
SEQFOL D score					
PMF	0.99	1.00	0.24	0.28	0.99
Verify	0.37	0.15	0.04	-0.15	0.23
Psi Blast	9.6e-31	1.4e-35	1.3e-25	1.3e-34	1.6e-35
END	303	324	495	547	565
STAR	158	186	298	382	429
CHAI	∢	∀	¥	٧	∢
PDB CD	1168	11f6	11f6	1466	1116
S B S	1801	1801	1801	1801	1801

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PDB annotation	FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG I; TRANSCRIPTION INITIATION,	INITIATOR ELEMENT, YY1, ZINCZ FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (PRANSCRIPTION PECH A PROMEMA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-YANG I; TRANSCRIPTION INITIATION.	INITIATOR ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-PROTEIN	(TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	The AMECUITATION INC. I AINC. I,	INTERPORT INTERPORT AND SINCE	FINGER PROTEIN, DNA-PROTEIN	RECOGNITION, 3 COMPLEX	(TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-YANG I;	TRANSCRIPTION INITIATION,	INITIATOR ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-PROTEIN	RECOGNITION, 3 COMPLEX	(TRANSCRIPTION BEGIN ATTONOMA)	COMPLEX (TRANSCRIPTION
Сонтроинд		YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA;	CHAIN: A, B;	YY1; CHAIN: C; ADENO-	ASSOCIATED VIKUS PS INITIATOR ELEMENT DNA:	CHAIN: A, B;				YY1; CHAIN: C; ADENO-	ASSOCIATED VIKUS PS	CHAIN: A B:	(7 t)				YY1; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;				YY1; CHAIN: C; ADENO-
SEQFOL D score				92.90																				
PMF		1.00				_				1.00	_						1:00				_			1.00
Verify score		0.25								0.35							0.15							0.17
Psi Blast		6e-43		7.5e-48						7.5e-48							7.5e-51							1.6e-32
END		590		267						294							322							322
STAR T AA		157		159						186							217				_			221
CHAI N ID		3		c						o o										_				C
PDB TD		Iubd		Inbd						Pqn1							lubd							Inpq
SEQ No. 10		1801		1801						1801							1801							1801

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PDB annotation	REGULATIONDNA) YING-YANG 1; TRANSCREPTON NITIATION, INTIATOR ELEMENT, YY, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIFTON) REGULATION(NA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) TYNG-YANG I; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YYI, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YNG-YNO I; TRANSCRIPTION INITIATION, INITIATION, INITIATION, INITIATION, ENGER RECOGNITION, 3 COMPLEX (TRANSCRIPTION), 3 COMPLEX (TRANSCRIPTION), 4 COMPLEX (TRANSCRIPTION), 5 COMPLEX	COMPLEX (TRANSCRIPTION) REGULATION/UNA YING-YANG 1; TRANSCRETION INITIATION, INITIATION, INITIATION, ETHORE REMENT, YY1, ZINC 2 FINGER PROTEIN, DAM-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRETION)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG I; TRANSCRIPTION INITIATION,
Coumpound	ASSOCIATED VIRUS PS INITIATOR BLEMBNT DNA; CHAIN: A, B;	VYI; CHAIN: C, ADENO- ASSOCIATED VIRUS PS INITIATOR ELEMENT DIA; CHAIN: A, B;	VYI; CRANI: C, ADENO- ASSOCIATED VIRUS PS NITIATOR ELEMENT DIA; CHAIN: A, B;	YYI; CHANY: C, ADBYO. SSOCIATED VIRUS PS. INITIATION ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INTIATOR ELEMENT DNA;
SEQFOL D score					
PMF		66:0	-0.02	0.64	0.36
Verify		-0.16	0.04	0.23	0.26
Psi Blast		3.2e-26	1.66-24	1.5e-30	6.4e-29
END AA		377	453	209	481
STAR T AA		249	305	351	360
CHAI N ID		ပ	ပ	ပ	၁
FDB CI		lubd	Iubd	1ubd	Jubd
SEQ ID NO:		1801	1801	1801	1801

SEQ PDB CHA STAR END Fil Blast Verify PMF StOPOL Coumpound PDB annotation PDB annotation No. 10 TAA AA AA AA Seore Score D Score CHAIN: A. B.; Filled PMF SCOGNITION SCORE PMTIATOR ELEMENT, YYI, ZINCZ PMTIATOR SCOGNITION SCORE PMTIATOR SCOGNITION SCORE PMTIATOR SCORE SCO						
PDB CHAI STAR END PM Blast Verify PMF Store	PDB annotation	INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULA TIONIDA)	COMPLEX (TRANSCRIPTION REGULATION/DAY) YING-YANG I; TRANSCRIPTION, INTIATON, INTIATON, INTIATON, ELBENDI, YY1, ZINC 2 FINCER, PROTEIN, DINA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION)	COMPLEX (TRANSCRIPTION REGULATION/DAY) YING-YANG I; TRANSCRIPTION, INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION	COMPLEX (TRANSCRIPTION REGILATION/DAY) YING-YANG I; TRANSCRIPTION, INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DINA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION TREGULATION/DNA)	
PDB CIAM STAR END Pit Blast Verify PARF	Coumpound	CHAIN: A, B;	YYJ; CIAIN; C; ADENO. SSOCIATED VIRUS PS INITIATOR ELEMENT DNA; CHAIN; A, B;	YYI; CHAIN: C, ADBNO- SASCATABD VIRUS PS INITIATOR ELEMENT DIN; CHAIN: A, B;	YYI; CIAIN: C; ADBNO- SSCOCATED YRUS P5 INITATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX(TRANSCRIPTION REGULATIONIDNA) TRAMTRACK PROTEIN (TWO ZINC-FINGER PEPTIDE) COMPLEXED WITH 2DRP 3
PDB CHA STAR END Fyl Blast Verify	SEQFOL D score					
PDB CHA STAR EAD Fu Bast	PMF		0.65	1.00	86.0	0.10
PB CEAN STAR END	Verify		0.07	0.30	-0.10	0.53
PDB CHA STAR PDB N D T AA			3.26-31	4.5e-40	8e-34	30-18
100 100			509	565	565	377
100 100d 100d 100d 100d 100d 100d 100d	STAR		387	454	464	294
	CHAI N ID		o	U	v	۷
NO DE 1881 1881 1881 1881 1881 1881 1881 1	PDB 110		1ubd		Iubd	2drp
	SEQ NO. ID		1801	1801	1801	1801

PDB annotation		LII; COMPLEX (DNA-BINDING C, D; PROTEINDNA) FIVE-TINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEINDNA)	LII; COMPLEX (DNA-BINDING C, D; PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)		E.J.; COMPLEX (DNA-BINDING C, D; PROTEINDNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEINDNA)	ELI; COMPLEX (DNA-BINDING C, D; PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	ELI; COMPLEX (DNA-BINDING C, D; PROTEINDINA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEINDNA)			4
Coumpound	DNA 2DRP 4	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GL/1; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GL/11; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLJI; CHAIN: A; DNA; CHAIN: C, D;	
SEQFOL D score		100.58								
PMF			1.00	0.90	0.81	0.49	-0.02	0.87	0.75	
Verify			0.25	0.15	10.0	0.11	0.15	0.40	0.25	
Psi Blast		1.1e-58	3e-57	1.1c-58	3.2e-23	1.1e-37	8e-30	6.4e-32	1.5e-48	
END		296	596	322	404	511	508	536	565	17.0
STAR		157	157	185	249	297	360	424	428	, 44
CHAI N ID		¥	¥	4	¥	٧	¥	Y	Ą	
PDB UD		2gli	2gli	2gli	2gli	2gli	2gli	2gli	2gli	
SEQ No.		1801	1801	1801	1801	1801	1801	1801	1801	.00.

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PDB annotation	PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)		LECTIN CL.QPDWG; 1AFB 7 C-TYPE LECTIN, CALCIUM-BINDING PROTEIN 1AFB 22	SUGAR BINDING PROTEIN C-TYPE LECTIN, CRD, SP-D, COLECTIN,	LUNG SURFACTANT, SUGAR BINDING PROTEIN	NK CELL NK CELL, RECEPTOR, C- TYPE LECTIN, C-TYPE LECTIN- LIKE, NKD	NK CELL NR CELL, RECEPTOR, C- TYPE LECTIN, C-TYPE LECTIN- LIKE NKD	COLLAGEN BINDING PROTEIN IX-	BP; IX-BP; COAGULATION FACTOR IX-BINDING, HETERODIMER,	VENOM, HABU 2 SNAKE, C-TYPE	LECTIN SUPERFAMILY, COLLAGEN BINDING PROTEIN	MEMBRANE PROTEIN SP.A; SP.	A:PHOSPHOLIPID MOLOLAYER COMPLEX	SIGNALING PROTEIN HEPATIC	SIGNATING PROTEIN HEPATIC	LECTIN HI; C-TYPE LECTIN CRD	HEMATOPOIETIC CELL RECEPTOR	ACTIVATION INDUCER MOLECULE (AIM), EA 1, HEMATOPOIETIC CELL
Coumpound	CHAIN: A; DNA; CHÁIN: C, D;		MANNOSE-BINDING PROTEIN- A; 1AFB 4 CHAIN: 1, 2, 3; 1AFB 5	LUNG SURFACTANT PROTEIN D; CHAIN: A, B, C;		CD94; CHAIN: NULL;	CD94; CHAIN: NULL;	COAGULATION FACTOR IX-	BINDING PROTEIN A; CHAIN: A; COAGULATION FACTOR IX-	BINDING PROTEIN B; CHAIN:	В;	SURFACTANT PROTEIN A;	CHAIN: A;	ASIALOGLYCOPROTEIN	ASIALOGI YCOPROTRIN	RECEPTOR 1; CHAIN: A;	EARLY ACTIVATION ANTIGEN	CD69; CHAIN: A;
SEQFOL D score			59.81			74.73		62.79										
PMF				0.83			86.0					0.18		1.00	0.48		0.65	
Verify score				0.35			0.57					90:0		0.47	0.35		62.0	
Psi Blast			1.5e-21	3e-31		4.5e-29	4.5e-29	8e-25				1.2e-27		1.5e-28	1.6e-28		1.5e-27	
END			252	249		253	251	250				249		250	252		250	
STAR T AA			6	118		123	126	125				103		126	126		125	
CHAI N ID			_	V				A				<		A	V		Ą	
PDB ID			lafb	1008		1b6e	1b6e	16j3				1du8		1dv8	ldv8		le87	
SEQ No:			1802	1802		1802	1802	1802				1802		1802	1802		1802	

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PDB annotation	RECEPTOR, LEUCOCYTE, C-TYPE LECTIN-LIKE, 2 NKD, KLR	C-TYPE LECTIN ALPHA-HELICAL COILED-COIL 1HUP 12	COAGULATION FACTOR BINDING	IX/X-BP COAGULATION FACTOR	BINDING, C-TYPE LECTIN, GLA-	MOTIF, LOOP EXCHANGED DIMER	COAGULATION FACTOR BINDING	IX/X-BP COAGULATION FACTOR	BINDING, C-TYPE LECTIN, GLA-	DOMAIN 2 BINDING, C-TYPE CRD	MOTIF, LOOP EXCHANGED DIMER	PANCREATIC STONE INHIBITOR PANCREATIC STONE INHIBITOR	LECTIN	METAL BINDING PROTEIN	PANCREATIC STONE PROTEIN, PSP;	PANCREATIC STONE INHIBITOR,	LITHOSTATHINE	METAL BINDING PROTEIN	PANCREATIC STONE PROTEIN, PSP;	PANCREATIC STONE INHIBITOR,	LITHUSTATHINE	COMPLEX (NK RECEPTOR/MHC	CLASS I) H-2 CLASS I	HISTOCOMPATIBILITY ANTIGEN,	B2M; NK-CELL SURFACE	GLYCOPROTEIN YE1/48, NK CELL,	INHIBITORY RECEPTOR, MHC-I, C.	TYPE LECTIN-LIKE, 2	HISTOCOMPATIBILITY, B2M, LY49,
Coumpound		MANNOSE-BINDING PROTEIN; 1HUP 4 CHAIN; NULL; 1HUP 5	COAGULATION FACTORS	IX/X-BINDING PROTEIN;	CHAIN: A, B, C, D, E, F;		COAGULATION FACTORS	IX/X-BINDING PROTEIN;	CHAIN: A, B, C, D, E, F;			LITHOSTATHINE; CHAIN:		LITHOSTATHINE; CHAIN: A;				LITHOSTATHINE; CHAIN: A;				MHC CLASS I H-2DD HEAVY	CHAIN; CHAIN: A; BETA-2-	MICROGLOBULIN; CHAIN: B;	HIV ENVELOPE	GLYCOPROTEIN 120 PEPTIDE;	CHAIN: P; LY49A; CHAIN: C, D;		
SEQFOL D score		63.07	65.37				61.47					96.78						74.13											
PMF														98.0								09.0							
Verify														0.75								09'0							
Psi Blast		3e-27	1e-24				6e-25					3e-25		3e-28				3e-28				1.5e-30							
END		249	250				252					252		252				252				253							
STAR T AA		86	125				125					126		114				114				123							
CHAI			¥				m							A				<				ر د							
10 a		1hup	lixx				lixx					≝		1qdd				1qdd			1	1903							
SEQ ID NO:		1802	1802				1802					1802		1802			- 1	1802				1802							

PDB annotation	COMPIEZ (NR RECEPTORAGE) CLASS) RE-OCLASS I HISTOCOMPATIBILITY ANTIGEN, BAM, NACELL SURFACE GLYCOPROTEIN YEL48, NK CELL, NHBHOTON RECEPTOR, MHC-I, C. TYPE LECTIVALIKE, Z. HISTOCOMPATIBILITY, BAM, LY49, LY49,	LECTIN SUB-MBP-C; IRDL 9 C-TYPE LECTIN, CALCIUM-BINDING PROTEIN IRDL 20		ANTIFREEZE PROTEIN RECOMBINANT SEA RAVEN PROTEIN, SOUTION BACKBONE FOLD, C. 2 TYPE LECTIN, ANTIFREEZE PROTEIN		LECTIN CL-QPDWG; IAFB 7 C-TYPE LECTIN, CALCIUM-BINDING PROTISIN 14FB 22	SUGAR BINDING PROTEIN C-TYPE LECTIN, CRD, SP-D, COLECTIN, ALPHA-HELICAL COLLED- 2 COIL, LUNG SURFACTANT, SUGAR
Coumpound	MEC CASS I, FAZDD HEAVY CHAIN, CHAIN, A; BETA-2, MICROGLOBULIN, CHAIN: B; HI SINTELOR GLYCOPROTEN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D;	MANNOSE-BINDING PROTEIN- C; IRDL 6 CHAIN: 1, 2; IRDL 7	LECTIN MANNOSE-BINDING PROTEIN A (CLOSTRIPAIN FRAGMENT) (CL-MBP-A) IRTM 3 IRTM 96	SEA RAVEN TYPE II ANTIFREEZE PROTEIN; CHAIN: A;	LECTIN MANNOSE-BINDING PROTEIN A (LECTIN DOMAIN) COMPLEX WITH 2MSB 3 CALCIUM AND GLYCOPEPTIDE 2MSB 4	MANNOSE-BINDING PROTEIN- A; IAFB 4 CHAIN: 1, 2, 3; IAFB 5	LUNG SURFACTANT PROTEIN D; CHAIN: A, B, C;
SEQFOL D score		61.44	63.45		61.86	60.17	
PMF	0.43			0.41			0.83
Verify	0.81			0.52			0.35
Psi Blast	1.3e-27	1.2e-26	4.5e-23	1.3e-29	1.3e-25	1.56-21	3e-31
END	253	251	252	250	251	291	288
STAR T AA	130	136	68	123	136	127	157
CHAI N ID	Q	-	1	٧	4	_	<
PDB	1903	Irdi	Irtm	2afp	2msb	lafb .	1908
SEQ NO:	1802	1802	1802	1802	1802	1803	1803

PDB annotation	BINDING PROTEIN	NK CELL NK CELL, RECEPTOR, C- TYPE LECTIN, C-TYPE LECTIN- LIKE, NKD	NK CELL NK CELL, RECEPTOR, C- TYPE LECTIN, C-TYPE LECTIN- LIKE, NKD	COLLAGEN BINDING PROTEIN IX- BP; IX-BP; COAGULATION FACTOR IX-BINDING, HETERODIMER,	VENOM, HABU 2 SNAKE, C-TYPE LECTIN SUPERFAMILY, COLLAGEN BINDING PROTEIN	COLLAGEN BINDING PROTEIN IX- BP: IX-BP: COAGULATION FACTOR	IX-BINDING, HETERODIMER, VENOM, HABU 2 SNAKE, C-TYPE	LECTIN SUPERFAMILY, COLLAGEN BINDING PROTEIN	MEMBRANE PROTEIN C-TYPE LECTIN-LIKE DOMAINS	MEMBRANE PROTEIN SP-4; SP-	A:PHOSPHOLIPID MOLOLAYER COMPLEX	SIGNALING PROTEIN HEPATIC	SIGNALING PROTEIN HEPATIC	LECTIN HI; C-TYPE LECTIN CRD	HEMATOPOIETIC CELL RECEPTOR ACTIVATION INDUCER MOLECULE	(AIM), EA 1, HEMATOPOIETIC CELL RECEPTOR, LEUCOCYTE, C-TYPE
Coumpound		CD94; CHAIN: NULL;	CD94; CHAIN: NULL;	COAGULATION PACTOR IX- BINDING PROTEIN A; CHAIN: A; COAGULATION FACTOR IX-	BINDING PROTEIN B; CHAIN: B;	COAGULATION FACTOR IX- BINDING PROTEIN A: CHAIN:	A; COAGULATION FACTOR IX- BINDING PROTEIN B; CHAIN:	á	FLAVOCETIN-A: ALPHA SUBUNIT; CHAIN: A; FLAVOCETIN-A: BETA SUBUNIT: CHAIN: B	SURFACTANT PROTEIN A;	CHAIN: A;	ASIALOGLYCOPROTEIN RECEPTOR 1: CHAIN: 4:	ASIALOGLYCOPROTEIN	RECEPTOR I; CHAIN: A;	EARLY ACTIVATION ANTIGEN CD69; CHAIN: A;	
SEQFOL D score		73.97		10.89												
PMF			86'0			0.48			-0.06	81.0		0.46	1.00		0.65	
Verify			0.57			0.16			0.38	90.0		0.13	0.47		67.0	
Psi Blast		4.5e-29	4.5e-29	1e-24		1e-24			4.5e-24	1.2e-27		4.8e-25	1.5e-28		1.5e-Z/	
END		292	290	289		288			290	288		288	289		582	
STAR T AA		162	165	164		165			165	142		165	165		<u>\$</u>	
CHAI N ID				٧		V			œ	٧		٧	4	1	<	
PDB		1pee	1996	Ibj3		16j3			lc3a	1du8		ldv8	ldv8		- es/	
SEQ NO:		1803	1803	1803		1803			1803	1803		1803	1803		1803	

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PDB annotation	LECTIN-LIKE, 2 NKD, KLR	LECTIN, MANNOSE RECEPTOR	C-TYPE LECTIN ALPHA-HELICAL COLLED-COIL 1HUP 12	C-TYPE LECTIN ALPHA-HELICAL	COLLED-COIL 1HUP 12	COAGULATION FACTOR BINDING	IX/X-BP COAGULATION FACTOR	BINDING, C-TYPE LECTIN, GLA-	MOTIF. LOOP EXCHANGED DIMER	COAGULATION FACTOR BINDING	IX/X-BP COAGULATION FACTOR	BINDING, C-TYPE LECTIN, GLA-	DOMAIN 2 BINDING, C-TYPE CRD	MOTIF, LOOP EXCHANGED DIMER	COAGULATION FACTOR BINDING	IX/X-BP COAGULATION FACTOR	BINDING, C-TYPE LECTIN, GLA-	DOMAIN 2 BINDING, C-TYPE CRD	MOTIF, LOOP EXCHANGED DIMER	COAGULATION FACTOR BINDING	IXX-BP COAGULATION FACTOR	BINDING, C-TYPE LECTIN, GLA-	DOMAIN 2 BINDING, C-TYPE CRD	MOTIF, LOOP EXCHANGED DIMER	PANCREATIC STONE INHIBITOR	PANCREATIC STONE INHIBITOR,	LECTIN	PANCREATIC STONE INHIBITOR	PANCKEALIC STONE INHIBITOR, LECTIN	METAL BINDING PROTEIN
Coumpound	144 CB CBITAGE MANDIOGE	RECEPTOR; CHAIN: A, B;	MANNOSE-BINDING PROTEIN; 1HUP 4 CHAIN: NULL; 1HUP 5	MANNOSE-BINDING PROTEIN;	HUP 4 CHAIN: NULL; 1HUP 5	COAGULATION FACTORS	IXX-BINDING PROTEIN;	CHAIN: A, B, C, D, E, F;		COAGULATION FACTORS	IX/X-BINDING PROTEIN;	CHAIN: A, B, C, D, E, F;			COAGULATION FACTORS	IX/X-BINDING PROTEIN;	CHAIN: A, B, C, D, E, F;			COAGULATION FACTORS	IX/X-BINDING PROTEIN;	CHAIN: A, B, C, D, E, F;			LITHOSTATHINE; CHAIN:	NULL		LITHOSTATHINE; CHAIN:	NOLL	LITHOSTATHINE; CHAIN: A;
SEQFOL D score			63.43			65.74									61.53													67.30		
PMF	90.0	CK:0		0.40						0.48										0.48					68.0					0.86
Verify	0.60	70:0		0.33						0.32										0.38					0.77					0.75
Psi Blast	1 60.06	1.36-23	3e-27	3e-27		le-24				1e-24					6e-25					6e-25					3e-25			3e-25		3e-28
END AA	000	997	288	289		289				288					291					290					291			291		291
STAR T AA	16.6	COT	150	164		164				165					164					165			_		165			165		153
CHAI N ID		A				¥				V					В					m										A
PDB ID	Tamp 1	282	dnyl	Thup		lixx				lixx					lixx					XX			_		=			Ħ		19dd
SEQ NO:	1003	1002	1803	1803		1803				1803					1803					1803					1803		0000	1803		1803

Coumpound PDB annotation		SEA RAVEN TYPE II AVITREEZE PROTEIN, CHAIN: RECOMBINANT SEA RAVEN A; FROTEIN, SOLUTION BACKBONE PODLO, CA TYPE LECTIN, ANTIPREEZE PROTEIN ANTIPREEZE PROTEIN	PROTEIN MANNOSE BRÜDING PROTEIN MANNOSE BRÜDING COMPLEX WITH BAKSB 3 GLYCOPETIDE DAKSB 4	ECTIN MANNOSE-BINDING PROTEIN A (LECTIN DOMAIN) COMPLEX WITH BANSB 3 GLYCCHTM AND GLYCCHTM AND	SERINE/THREONINE HYDROLASE CALCINEURIN; PHOSPHATASE 2B; CHAIN: A, HYDROLASE, PHOSPHATASE, IMMUNOSUPPRESSION B;		Z - 9	m 6	m 0 0
	3 IRTM 96	SEA RAVEN TYPE II ANTIFREEZE PROTE A;	LECTIN MANNOSE-BINE PROTEIN A (LECTIN DO) COMPLEX WITH 2MSB 3 CALCIUM AND GLYCOPEPTIDE 2MSB 4	LECTIN MANNOSE-BINT PROTEIN A (LECTIN DOI COMPLEX WITH 2MSB 3 CALCIUM AND GLYCOPEPTIDE 2MSB 4	SERINE/THREONINE PHOSPHATASE 2B; C B;		CALCIUM-BINDING PROTEI CALMODULIN COMPLEXED WITH CALMODILIN-BINDI DOMAIN OF ICDM 3 CALMODULIN-DEFENDENT BEOTERN WAN OF IT ONLY	CALCUM-BUNDING PROTEIN CALMODULIN COMPLEXEDS CALMODULIN-BUNDIN DOMANI OF COMING PROCEEN KINASE II COMA CALMODULIN DEPENDENT CALMODULIN (VERTEBRAT ICLL 3	CALCUMABIND CALMODULING WITH CALMOD DOMARIO OF ICE CALMODULING CALMODULING ICLE 3 ICLE 3 ICLE 3 ICLE 4 ICLE ARRIVED CALMODULING ICLE ARRIVED CALMODULING
SEQFOL D score			61.86						
PMF		0.41		0.54	0.87	98.0		0.49	0.60
Verify score		0.52		0.57	0.10	-0.07		-0.04	-0.04
Psi Blast		1.3e-29	1.3e-25	1.3e-25	4.8e-24	1.6e-29		8e-36	8e-36 8e-32
END AA		289	290	288	08			81	81 81
STAR T AA		162	175	176	_	_			
CHAI N ID		<	∀	4	В	¥			
PDB CI		2afp	2msb	2msb	Iaui	lcdm		lcll	loll lomf
SEQ E E		1803	1803	1803	1804	1804		1804	1804

PDB annotation	A; TRANSPORT PROTEIN CALCIUM BINDING, EF HAND, FOUR-HELIX BUNDLE	ULL; CACLOW-REGULATD MUSCLE CONTRACTION AUSCLE CONTRACTION AUSCLE CONTRACTION AUSCLE RINDING, TROPONIN, E. P. BAND, 2 PREGULATION CALCIUM- REGULATION Y DOMAN, CALCIUM- REGULATION Y DOMAN CALCIUM- CONTRACTION	ITOP 3	TEIN 3.5 OF E) ITRC	A; CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEXICALCIUM-BINDING PROTEIN/PEPTIDE)	ô	IAIN: Q. COMPLEX (NUCLEAR 2 B°; PROTEIN/RIA), COMPLEX (NUCLEAR PROTEIN/RIA), RIA, SNRAP, RIBONUCLEOPROTEIN	A; CELL ADHESION LEUCINE RICH
Coumpound	CALMODULIN; CHAIN: A;	TROPONIN G; CHAIN: NULL;	CONTRACTILE SYSTEM PROTEIN TROPONIN C 1TOP 3	CALCIUM BINDING PROTEIN CALMODULIN (/IR=2=CS PRAGMENT COMPRISING RESIDUES 78 - 148 ITRC 3 OF THE INTACT MOLECULE) ITRC 4	CALMODULIN; CHAIN: A; RS20; CHAIN: B;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A; CHAIN: A, C; U2 B°; CHAIN: B, D;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	INTERNALIN B; CHAIN: A;
SEQFOL D score								
PMF	68'0	1.00	56'0	86'0	0.98	1.00	0.99	86.0
Verify	0.39	0.23	0.25	0.52	0:30	0.60	0.58	0.57
Psi Blast	8e-30	1.6e-24	1.6e-24	1.4e-30	3.2e-35	80-24	8e-24	6.4e-34
END	18	18	81	81	82	250	250	227
STAR T AA	14	-	_	12	1	114	114	44
CHAI	4			∢	٧	₹	υ	٧
PDB	1731	Itef	Itop	Itro	lvrk	la9n	la9n	1d0b
SEQ UD NO:	1804	1804	1804	1804	1804	1806	1806	1806

PDB annotation	ADHESION	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION	TRANSFERASE CRYSTAL	STRUCTURE, RAB GERANYLGERANYLTRANSFERASE,	2.0 A 2 RESOLUTION, N-	FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT		TRANSFERASE CRYSTAL STRUCTURE, RAB	GERANYLGERANYLTRANSFERASE,	2.0 A 2 RESOLUTION, N-	FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT		CONTRACTILE PROTEIN LEUCINE.	RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2	CHLAMYDOMONAS, FLAGELLA	CONTRACTILE PROTEIN LEUCINE-	RICH REPEAT, BETA-BETA-ALPHA	CHLAMYDOMONAS, FLAGELLA	CONTRACTILE PROTEIN LEUCINE-	RICH REPEAT, BETA-BETA-ALPHA	CHI AMYDOMONAS ET AGELLA	CHESTAL DOMOGRAS, LEAGUES	COMPLEX (HSP24/HSP70) HSP70, GRPE, MOLECULAR CHAPERONE,	NUCLEOTIDE EXCHANGE 2
Coumpound		INTERNALIN B; CHAIN: A;	RAB	GEKANYLGERANYLIKANSFE RASE ALPHA SUBUNIT;	CHAIN: A, C; RAB	GERANYLGERANYLTRANSFE RASE BETA SUBUNIT; CHAIN:	B,D;	RAB GERANYLGERANYLTRANSFE	RASE ALPHA SUBUNIT;	CHAIN: A, C; RAB	GERANYLGERANYLTRANSHE RASE BETA SUBUNIT; CHAIN:	B,D;	OUTER ARM DYNEIN; CHAIN:	A;		OUTER ARM DYNEIN; CHAIN:	À;		OUTER ARM DYNEIN; CHAIN:	Ą;			NUCLEOTIDE EXCHANGE FACTOR GRPE, CHAIN: A, B;	MOLECULAR CHAPERONE
SEQFOL D score																								
PMF score		1.00	66'0					0.88					0.78			0.46			10.0				0.11	
Verify		0.39	0.51					0.45					-0.40			-0.60			-0.30				-0.10	
Psi Blast		1.3e-32	3.2e-25					3.2e-17					3e-14			1.6e-28			3.2e-13				0.0015	
END		235	249					207					191			251			179		_		398	
STAR		25	132					84					111			125			73				250	
CHAI		V	A					∢					٧			<			V				4	
EDB CI		90P1	Idee					1dee					6sp1			1ds9			1ds9			ľ	Idkg	
SEQ NO.		1806	1806					1806					1806			1806			1806				1809	

_		Г		_		T		101	Γ
PDB annotation	FACTOR, COILED-COIL, COMPLEX (HSP24/HSP70)	ENDOCYTOSIS/EXOCYTOSIS NSEC1; PROTEIN-PROTEIN COMPLEX, MULTI-SUBUNIT	CONTRACTILE PROTEIN TRIPLE- HELIX COILED COIL, CONTRACTILE PROTEIN			HYDROLASE TARTRATE- RESISTANT ACID PHOSPHATASE; METAL PHOSPHATASE, HYDROLASE	HYDROLASE TARTRATE- RESISTANT ACID PHOSPHATASE; METAL PHOSPHATASE, HYDROLASE	HYDROLASE UTEROFERRIN, TRAP, PAP, TARTATE BERSITANT ACID PURPLE ACID PHOSPHATASE, TARTRATE RESISTANT ACID 2 PHOSPHATASE, METALLOBEXYME, UTEROFERRIN, HYDROLASE	HYDROLASE (PHOSPHORIC MONOESTER) PURPLE ACID PHOSPHATASE, HYDROLASE (PHOSPHORIC MONOESTER)
Coumpound	DNAK; CHAIN: D;	SYNTAXIN BINDING PROTEIN 1; CHAIN: A; SYNTAXIN 1A; CEAIN: B;	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;		LIGASE(SYNTHETASE) SERYL- TRNA SYNTHETASE (E.C.6.11.11) (SERINE-TRNA LIGASE) 1SES 3 COMPLEXED WITH SERYL-HYDROXAMATE- AMP 1SES 4	PURPLE ACID PHOSPHATASE; CHAIN: A;	PURPLE ACID PHOSPHATASE; CHAIN: A;	II PURPLE ACID PHOSPHATASB; CHAIN: A;	PURPLE ACID PHOSPHATASE; CHAIN: A, B, C, D;
SEQFOL D score						61.74		63.06	
PMF		-0.07	0.07		0.28		0.34		0.52
Verify		90.00	-0.12		0.21		-0.19		0.01
Psi Blast		30-08	7.5e-13		1.6e-05	4.5e-10	4.5e-10	0.00014	1.56-12
END AA		367	374		528	310	239	320	247
STAR T AA		143	102		439	32	39	38	10
CHAI		g g	<		∢	٧	∢	∢	∢
EDB EI		1dn1	Idun		lses	Ідћи	Iqhw	lute	4крр
SEQ No es		1809	1809		1812	1814	1814	1814	1814

PDB annotation		XXL-LEHAL PROTEIN; CHAIN: RAS-BINDING PROTEINRNA TRA A, B; PRA (5"- REGULATION REGULATION, RNP DOMAIN, RNA REGULATION, RNP DOMAIN, RNA ONLY OF TAXA, B. O. ONLY D. O.		METAL TRANSPORT MRPS, S100AS, CALGRANULIN A CALCUM, BINDING PROTEIN, CRYSTAL STRUCTURE, MAD, MIGRATION 2 INHBITOSY PACTOR, RELATED PROTEINS, S100 PROTEIN		NUCLEAR PROTEIN UI SNRNP A PROTEIN; RNA BINDING DOMAIN, NUCLEAR PROTEIN	NUCLEAR PROTEIN UI SNRNP A PROTEIN; RNA BINDING DOMAIN, NUCLEAR PROTEIN	RNA BINDING DOMAIN RNA BINDING DOMAIN RNA BENGGNITON MOTIF, RRM, 2 SPLICING INHIBITOR, RRS, 3 FRANKLATIONAL MUHBITOR, SEX 3 PETRANKLATIONAL NY CHROMOSOWE
Coumpound	Control of the contro	SXL-LEIHAL PROIEIN; CHAIN; A, B; RNA (5'- R(P*GP*UP*UP*GP*UP*UP* TREE DATESTORY	NUCLEOLIN RBD2; CHAIN: A;	MIGRATION INHIBITORY FACTOR-RELATED PROTEIN 8; CHAIN: A, B;	RAN-BINDING PROTBIN SEX- LETHAL PROTBIN (C. TERMINUS, OR SECOND: RNA- BINDING DOMAIN 18X1. 3 (RBD-2), RESIDUES 199-294 PLUS N-TERMINAL MET) 1SXL 4 (NMR, 17 STRUCTURES) 1SXL	UI SMALL NUCLEAR RIBONUCLEOPROTEIN A; CHAIN: NULL:	UI SMALL NUCLEAR RIBONUCLEOPROTEIN A; CHAIN: NULL;	SEX-LETHAL; CHAIN: A, B, C;
SEQFOL D score								
PMF		0.40	0.12	0.21	0.13	0.55	0.31	0.18
Verify score		-0.30	-0.15	0.07	-0.32	0.29	0.31	-0.10
Psi Blast		3.26-05	60-09.6	0.0045	3.2e-05	0.003	0.0093	6.4e-05
END	000	717	250	149	272	267	256	257
STAR T AA		3	180	101	195	188	561	\$61
CHAI		∢	A	<				⋖
202 CI		1/01	1fjc	1mr8	Isxl	2ula	2ula	3sxl
SEQ ID NO:	1	CIST	1815	1815	1815	1815	1815	1815

PDB annotation	DOSAGE COMPENSATION	N: HYDROLASE HOMODIMER, ALPHA/BETA HYDROLASE FOLD, DISUBSTITUTED UREA 2 INHIBITOR	N: HYDROLASE HOMODIMER, ALPHA/BETA HYDROLASE FOLD, DISUBSTITUTED UREA 2 INHIBITOR		DEHALOGENASE DEHALOGENASE, HYDROLASE	ELECTRON TRANSPORT ELECTRON TRANSPORT, IRON-SULFUR	ELECTRON TRANSPORT ELECTRON TRANSPORT, IRON-SULFUR	ELECTRON TRANSFER (IRON- SULFUR PROTEIN)	ELECTRON TRANSPORT TWO 4FE- 4S CLUSTERS	HYDROGENASE HYDROGENASE, CYTOCHROME C533, ELECTRON TRANSFER COMPLEX	ш	HYDROGENASE HYDROGENASE, CYTOCHROME C553, ELECTRON TRANSFER COMPLEX
Coumpound		EPOXIDE HYDROLASE; CHAIN: A, B;	EPOXIDE HYDROLASE; CHAIN: A, B;	PHOSPHONOACETALIDEHYDE HYDROLASE; CHAIN: A, B, C, D;	L-2-HALOACID DEHALOGENASE; CHAIN: NULL;	7-FE FERREDOXIN; CHAIN: NULL;	7-FE FERREDOXIN; CHAIN: NULL;	FERREDOXIN; ICLF 5 CHAIN: NULL ICLF 6	2[4FE-4S] FERREDOXIN; CHAIN; A	[FE]-HYDROGENASE (LARGE SUBUNIT); CHAIN: A; [FE]- HYDROGENASE (SMALL SUBUNIT); CHAIN: D;	CYTOCHROME C553; CHAIN: E	FEJ-HYDROGENASE (LARGE SUBUNIT); CHAIN: A; [FE]- HYDROGENASE (SMALL SUBUNIT); CHAIN: D; CYTOCHROME C553: CHAIN: B
SEQFOL D score		,										
PMF		-0.14	0.05	0.64	-0.19	-0.19	-0.17	-0.17	-0.12	1.00		1.00
Verify		-0.00	-0.84	0.20	0.12	0.05	0.17	0.43	0.53	0.37		0.23
Psi Blast		3.2c-09	0.006	90-06	3e-10	8e-14	1.1e-10	1.1e-10	1.ee-11	6.4e-68		30-92
END		305	69	143	316	219	254	199	200	519		504
STAR T AA		172	39	38	28	137	176	137	137	136		173
CHAI N ID		<	m	₹					V	<		<
PDB		1ek1	leki	1fez	lzm	1bc6	1bc6	lelf	ldur	1e08		1e08
SEQ NO:		1819	1819	6181	1819	1820	1820	1820	1820	1820		1820

_		_	_		_		_		_	_	_	_	-	_	_	_	_				_	_	_			-
OXIDOREDUCTASE OXIDOREDUCTASE	OXIDOREDUCTASE OXIDOREDUCTASE	HYDROGENASE FE-ONLY	CPXSTA11OGPAPHY HYDROGENE	2 METABOLISM, PERIPLASM	HYDROGENASE FE-ONLY	HYDROGENASE, X-RAY	CRYSTALLOGRAPHY, HYDROGENE	Z METABOLISM, PERIFLASM	HYDROGENASE FE-ONLY	HYDROGENASE, X-RAY	CRYSTALLOGRAPHY, HYDROGENE	Z METADOLISM, FEMILENSM		STRUCTURAL PROTEIN TWO	REPEATS OF SPECTRIN, ALPHA	HELICAL LINKER REGION, 22	TANDEM 3-HELIX COILED-COILS,	STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TWO	REPEATS OF SPECTRIN, ALPHA	HELICAL LINKER REGION, 22	IANDEM 3-HELIX COLLED-COLLS,	STRUCTURAL PROTEIN	CONTRACTILE PROTEIN TRIPLE.	CONTRACTILE PROTEIN	CONTRACTILE PROTEIN TRIPLE.
PERIPLASMIC HYDROGENASE 1; CHAIN: A;	PERIPLASMIC HYDROGENASE 1; CHAIN: A;	FE-ONLY HYDROGENASE	S T. FF. ONLY HYDROGENASE	CARGER SUBUNIT); CHAIN: 1, M:	FE-ONLY HYDROGENASE	(SMALLER SUBUNIT); CHAIN:	S, T; FE-ONLY HYDROGENASE	(LARGER SUBUNIT); CHAIN: L,	PE-ONLY HYDROGENASE	(SMALLER SUBUNIT); CHAIN:	S, I; FE-ONLY HYDROGENASE	M;		ALPHA SPECTRIN; CHAIN: A,	B, C;				ALPHA SPECTRIN; CHAIN: A,	B, C;				HUMAN SKELETAL MUSCLE AI PHA-ACTININ 2: CHAIN: A:	the transfer of the transfer of	HUMAN SKELETAL MUSCLE
232.77		223.69																						52.84		
	1.00				1.00				1.00					0.01					0.36							0.43
	0.33				0.40				0.61					-0.18					-0.09							-0.34
1.4e-85	1.4e-85	4.5e-92			3.2e-68				4.5e-92					6e-99					1.5e-07					9e-12		9e-12
574	572	524			619				504					344					202					305		340
-	69	117			122				173					104					21					24		56
A	V	1			7									٧					4					∢		٧
Heh	1feh	Thfe			lhfe				lhfe					1cm					Icun					Idm		Iduu
1820	1820	1820			1820				1820					1821					1821					1821		1821
	1ish A 1 374 1.46-85 232.77 PERIPLASMIC HYDROGENASE 1; CHAIN: A; 1; CHAIN: A;	15th A 1 574 14e-85 232.77 PERPLASNIC HYDROGENASE 15th A 69 572 14e-85 0.33 1.00 PERPLASNIC HYDROGENASE PERPLASNIC HYDROGENASE 1.00 PERPLASNIC HYDROGENASE	15th A 1 574 14-85 222.77 EFREPLASMIC HYDROGENASE 15th A 69 572 14-85 0.33 1.00 FREPLASMIC HYDROGENASE 15th A 572 45-92 223.69 FE-ONLY HYDROGENASE 15th A 572 45-92 1.00 1	15th A 1 574 14e-85 22.2.7 PERPLASMIC HYDROGENASE 15th Art	15th A 1 574 14e-85 232.77 15th PRIRPLASMIC HYDROGENASE 15th A 69 572 14e-85 0.33 1.00 1.05 1.00 1.05 1.00 1.05 1.00 1.05 1.00 1.05 1.00 1.05 1.00 1.05 1.00 1.05 1.00 1.05 1.00 1.05 1.00 1.05 1.00 1.05 1.00 1.05 1.00 1.05 1	15th A 1 574 14e-85 22.27 PERPLASMIC HYDROGENASE 1.04645 1	15th A 1 374 14e-85 232.77 15th PREPLASAGE HYDROGENASE 15th A 69 572 14e-85 0.33 1.00 1.0th PANGE HYDROGENASE 15th A 545-92 1.00 1.0th PANGE HYDROGENASE 1.0th PANGE	15th A 1 374 14e-85 222.77 15TPROGENASE 15TPLANG HYDROGENASE 15TPLANG HYD	15th A 1 374 14e-85 232.77 19FBPLPASMOTHYDROGENARE 15th A 69 372 14e-85 0.33 1.00 1. CHAUR. A 1.	15th A 1 374 14e-85 1.22.77 1.05.05.04.0EPR PASAGE (HYDROGENASE FIfth A 69 372 14e-85 0.33 1.00 1.05.04.04.0. 1.05.04.	15th A 1 374 14e-85 232.77 15th A 572 14e-85 0.33 1.00 27.7 15th A 572 14e-85 0.33 1.00	15th A 1 374 14e-85 132.77 17th A 10 17th A 17th	15th A 1 574 14e-85 1.22.77 1.05.05.05.05.05.05.05.05.05.05.05.05.05.	15th A 1 574 14e-85 232.77 1FBEPLASMIC HYDROGENASE 15th A 69 572 14e-85 0.33 1.00 1.CHARN. A. 1.CHAR	15th A 1 374 14e-85 1.22.77 1.05.47 1.05	15th A 1 374 14e-85 232.77 15th PREPLASMIC HYDROGENASE 15th A 69 572 14e-85 0.33 1.00 1.0th PASMIC HYDROGENASE 15th	15th A 1 574 14e-85 1.22.77 1.05.47 1.05	15th A 1 374 14e-85 232.77 1FBERPLASMIC HYDROGENASE 116th A 69 572 14e-85 0.33 1.00 275 1FERPLASMIC HYDROGENASE 110th A 69 572 14e-85 0.33 1.00	15th A 1 574 14e-85 1.22.77 1.05.00 1.05	15th A 1 374 14e-85 232.77 15th PREPLASMIC HYDROGENASE 15th A 69 572 14e-85 0.33 1.00 275 15th PROPASMIC HYDROGENASE 15th PROPASM	15th A 1 374 14e-85 1.25 1.05	15th A 1 374 14e-85 1.20 1.0	15th A 1 374 14e-85 1.02.77 1.05.07 1.05.07 1.05.05 1.05	15th A 1 574 14e-85 1.20 1.0	15th A 1 374 14e-85 1.00 1.0	15th A 1 574 14e-85 0.33 1.00 1.

PDB CHAI STAR END Psi Blast ID NID TAA AA	STAR END TAA AA	END			last	Verify score	PMF	SEQFOL D score	Coumpound	PDB annotation
									ALPHA-ACTININ 2; CHAIN: A;	HELIX COULED COIL, CONTRACTILE PROTEIN
latt L 29 125 9c-08	29 125	125		80-96				51.57	ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/NHIBITOR) AUTOPROCHEMBIN IN, HYDROLASE, SERINE PROTEINASE, PLASMA CALCIUM BINDING, 2 GLYCOROTEIN, COMPLEX (BLOOD)
1bx7 45 113 6e-11 1.12	113 6e-11	113 6e-11	6e-11		1.12		-0.15		HIRUSTASIN; CHAIN: NULL;	COGGULATIONINHIBITOR) ANTI-COAGULANT ANTI- COAGULANT, PIETIDIC INHIBITORS, CONFORMATIONAL 2 FLEXIBLITY, SERINE PROTEASE DAHRITOR
Ic2a A 36 165 1.4e-26 0.53	36 165 1.4e-26	165 1.4e-26	1.4e-26		0.53		-0.03		BOWMAN-BIRK TRYPSIN INHIBITOR; CHAIN: A	HYDROLASE INHIBITOR ALL-BETA STRUCTURE, HYDROLASE INHIBITOR
1c2a A 4 126 1.5e-19 0.87	4 126 1.5e-19	126 1.5e-19	1.5e-19		0.87		-0.15		BOWMAN-BIRK TRYPSIN INHIBITOR; CHAIN: A	HYDROLASE INHIBITOR ALL-BETA STRUCTURE, HYDROLASE INHIBITOR
Idan L 2 135 7.5e-13 0,56	135 7.5e-13	135 7.5e-13	7.5e-13		0.56		-0.19		BLOOD COAGULATION FACTOR VIIA; CHAIN: I, II; SOLUBLE TISSUE FACTOR; CHAIN: T, IJ, D-PHE-PHE-ARG- CHLOROMETHYLKETONE CHLOROMETHYLKETONE	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
Idu3 A 2 77 7.5e-11 1.08	2 77 7.5e-11	77 7.56-11	7.56-11		1.08		-0.18		DEATH RECEPTOR 5; CHAIN: A, B, C, G, H, J; TNF-RELATED APOPTOSIS INDUCING LIGAND: CHAIN: D, E, F, J, K, L;	APOPTOSIS TRAIL, DR5, COMPLEX
1du3 A 31 125 4.5c-12 0.59	31 125 4.56-12	125 4.50-12	4.5e-12		0.59		-0.12		DEATH RECEPTOR 5; CHAIN: A, B, C, G, H, I; TNF-RELATED	APOPTOSIS TRAIL, DR5, COMPLEX

PDB annotation		APOPTOSIS TRAIL, DRS, COMPLEX	SERNE PROTEINASB COAGULATION FACTOR II; ESTOMODULN; TN, CD14 ANTIGEN; EGR-CMK SERINB PROTEINAS, EGR-LIKE SERINB PROTEINAS, EGR-LIKE DOMAINS,	ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX	PLANT PROTEIN TWO HOMOLOGOUS HEVEIN-LIKE DOMAINS	PLANT PROTEIN TWO HOMOLOGOUS HEVEIN-LIKE DOMAINS	PLANT PROTEIN TWO HOMOL OGOUS HEVEIN-LIKE DOMAINS	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA,
	.6			ANA	PLAI HOIV	PLAI HOM DOIN	HOM		 	_	Н
Coumpound	APOPTOSIS INDUCING LIGAND; CHAIN; D, E, F, J, K, L;	DEATH RECEPTOR 5; CHAIN: A, B, C, G, H, I; TNF-RELATED APOPTOSIS INDUCING LIGAND; CHAIN: D, E, F, J, K, L;	THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CIAIN: I, I, K, I, THROMBIN INHIBITOR L, GLU-L, GLY-L.	ARM; CHAIN: E, F, G, H;	AGGLUTININ ISOLECTIN VI; CHAIN: A	AGGLUTININ ISOLECTIN VI; CHAIN: A	AGGLUTININ ISOLECTIN VI; CHAIN: A	AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V; CHAIN: A:	AGGLUTININ ISOLECTIN VIAGGLUTININ ISOLECTIN V; CHAIN: A;	AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V; CHAIN: A;	AGGLUTININ ISOLECTIN VI/AGGLUTININ ISOLECTIN V;
SEQFOL D score											
PMF		-0.15	-0.14		-0.18	-0.12	0.16	0.17	0.11	0.10	-0.17
Verify		1.17	0.58		0.49	<u>=</u>	1.00	0.87	1.02	1.08	0.24
Psi Blast		6e-12	4.5e-11		1.4e-18	7.5e-19	1.40-18	1.5e-19	1.2c-19	1.5e-19	7.5e-17
END		96	155		1111	16	141	121	06	141	160
STAR T AA		6	47		12	4	. 22	61	4	52	75
CHAI N ID		٧	2004		A	Ą	٧	Ą	V	A	A
PDB ID		1du3	1dx5		lehd	lehd	1ehd	leis	1eis	leis	leis
SEQ No:		1822	1822		1822	1822	1822	1822	1822	1822	1822

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PDB annotation	SUPERANTIGEN	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN, SACCHARIDE BINDING	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN, SACCHARIDE BINDING	SUGAR BINDING PROTEIN UDA;	LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN, SACCHARIDE BINDING	SUGAR BINDING PROTEIN UDA:	LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN, SACCHARIDE	BINDING	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN	Old It I blo bhombar a barbar a	PROTEIN, CYTOKINE, SIGNALLING PROTEIN	SIGNALLING PROTEIN BINDING	PROTEIN, CYTOKINE, SIGNALLING PROTEIN	HORMONE RECEPTOR HORMONE	RECEPTOR, INSULIN RECEPTOR FAMILY	GLYCOPROTEIN GLYCOPROTEIN	GLYCOPROTEIN GLYCOPROTEIN	GLYCOPROTEIN GLYCOPROTEIN	SIGNALLING PROTEIN TYPE I RECEPTOR, STNFR 1: 1NCF 8
Coumpound	CHAIN: A;	AGGLUTININ ISOLECTIN I/AGGLUTININ ISOLECTIN V/ CHAIN: A;	AGGLUTININ ISOLECTIN I/AGGLUTININ ISOLECTIN V/ CHAIN: A;	AGGLUTININ ISOLECTIN	L'AGGLUTININ ISOLECTIN V/ CHAIN: A;	AGGLUTININ ISOLECTIN	VAGGLUTININ ISOLECTIN V/ CHAIN: A;		TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	THE PARTY OF STREET	RECEPTOR; CHAIN: A, B;	TUMOR NECROSIS FACTOR	RECEPTOR; CHAIN: A, B;	INSULIN-LIKE GROWTH	FACTOR RECEPTOR 1; CHAIN: A;	LAMININ; CHAIN: NULL;	LAMININ; CHAIN; NULL;	LAMININ; CHAIN: NULL;	TUMOR NECROSIS FACTOR RECEPTOR: INCF 4 CHAIN: A.
SEQFOL D score									62.34									82.39	50.41
PMF		-0.13	-0.18	0.11		-0.14				110	÷.	-0.14		-0.19		-0.15	-0.06		
Verify		0.40	1.10	1.04		19.0				0.70	0.70	0.63		0.40		0.65	1.13		
Psi Blast		36-18	91-99	3e-21		6e-18			7.5e-20	00.5	07-07/	6e-13		1.5e-28		1.2e-19	7.5e-27	7.5e-27	1.5e-12
END AA		121	06	141		160			141	175	3	128		178		178	155	157	171
STAR		12	2	52		62			10	2	1	3		4		43	4	+	*
CHAI N ID		¥	¥	V		A		!	٧		<	٧		A					∢
PDB CI		len2	len2	len2		len2			lext	Lores	- ICA	lext		ligr		1140	1klo	1klo	Incf
SEQ No. 10		1822	1822	1822		1822			1822	1000	7701	1822		1822		1822	1822	1822	1822

PDB annotation	BINDING PROTEIN, CYTOKINE INCP 19	SIGNALLING PROTEIN TYPE I RECEPTOR, STNFRI; INCF 8 BINDING PROTEIN, CYTOKINE INCF 19	EXTRACELLULAR MODULE OSTEDORETRI, SPACE, SECRETED PROTEIN ACIDIC AND EXTRACELLULAR MODULE, EXTRACELLULAR MODULE, ELYCOPROTEIN, ANT-ADHESIVE PROTEIN, 2 COLLAGEN BINDING,	SITE-DIRECTED MUTAGENESIS, GLYCOSYLATED 3 PROTEIN MODRES	COMPLEX (BLOOD COAGLATON/PHEITOR) COAGLATON/PHEITOR) COAGULATON/PHEITOR) CHRISTMAS PACTOR; COAPLEX, PHISTORY, ETWOOPHILA/PEGF; BLOOD COAGULATION, 2 PLASMA, SERNER PROTEASE, CALCIUM- BINDING HYDROLASE, 3 (CALCIUM- GI YCOPROTEN)	COMPLEX (BLOOD COAGUATION/HBITOR) CHRISTMAS PACTOR; COMPLEX INHIBITOR), ENWOPHILIA/PEGF, BLOOD COAGULATION, 2 PLASMA, SERNER PROTESAE, CALCILIA- BINDIA, HYDROLASIS, GALCILIA- GALVOPROTEIN	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR: COMPLEX.
Coumpound	B; INCF 5	TUMOR NECROSIS FACTOR RECEPTOR, INCF 4 CHAIN: A, B; INCF 5	BASEMENT MEMBRANE PROTEIN BM-40, CHAIN: A, B;		FACTOR IXA; CHAIN: C, L., D. PHE.PRO-ARO; CHAIN: I;	FACTOR IXA; CHAIN: C, L., D. PHE-PRO-ARG; CHAIN: I;	FACTOR IXA; CHAIN: C, L,; D- PHE-PRO-ARG; CHAIN: I;
SEQFOL D score						55.26	
PMF score		-0.14	-0.19		-0.20		-0.20
Verify		99.0	0.10		0.14		0.44
Psi Blast		1.5e-12	6e-26		36-23	3e-23	9e-14
END		155	171		179	178	123
STAR T AA		35	12		61	36	6
CHAI N ID		A	∢		_1	٦	7
EDB ED		Incf	Inub		1pfk	1pfx	1pfx
SEQ NO.		1822	1822		1822	1822	1822

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PDB annotation	INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3 GLYCOPROTEIN	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CIVESTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS	SERINE PROTEASE INHIBITOR PACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS	SERINE PRÓTEASE INHIBITOR PACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, TAROMBOSIS	SERING PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTENSIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE
Coumpound		ANTISTASIN; CHAIN: NULL;	ANTISTASIN; CHAIN: NULL;	ANTISTASIN; CHAIN: NULL;	ANTISTASIN; CHAIN: NULL;	AMISTASIN, CHAIN: NULL;
SEQFOL D score					63.90	
PMF		0.54	-0.06	0.11		-0.12
Verify		0.63	0.57	0.03		0.61
Psi Blast		1.2e-18	7.5e-21	7.56-25	7.5e-25	1.5e-18
END		134	147	176	180	117
STAR T AA		22	8	71	11.	∞
CHAI N ID						
EDB EDB		1sk2	Iskz	Iskz	Iskz	1sfz.
SEQ NO.		1822	1822	1822	1822	1822

PDB annotation	INHIBITOR, THROMBOSIS			ANTI-COAGULANT ANTI- COAGULANT, PEPTIDIC INHBITORS, CONFORMATIONAL 2 FLEXIBILITY, SERINE PROTEASE INHBITOR	APOPTOSIS TRAIL, DR5, COMPLEX									BLOOD COAGULATION FACTOR	COAGHI ATION FACTOR SERINE	PROTEINASE, EPIDERMAL 2	GROW HEACTOR LIKE DOMAIN
Coumpound		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	HIRUSTASIN; CHAIN: NULL;	DEATH RECEPTOR 5; CHAIN: A, B, C, G, H, I; TNF-RELATED APOPTOSIS INDUCING	LIGAND; CHAIN: D, E, F, J, K, L;	METALLOTHIONEIN CD-7 METALLOTHIONEIN-2 (ALPHA DOMAIN) (NMRS) IMHUA 2	METALLOTHIONER CD-7	METALLOTHIONEIN-2 (ALPHA DOMAIN) (/NMR\$) IMHUA 2	METALLOTHIONEIN CD-7	METALLOTHIONEIN-2 (ALPHA DOMAIN) (/NMR\$) 1MRTA 2	METALLOTHIONEIN CD-7	DOMAIN (NMRS) IMRTA 2	BLOOD COAGULATION	FACTOR AS; CEAIN: L, C;		
SEQFOL D score		65.701						65.07				63.47					
PMF			0.03	0.07	-0.12		1:00			1.00				0.10			
Verify score			0.57	0.23	0.07		0.40			0.49				0.34			
Psi Blast		66-30	3e-26	4.5e-20	3c-08		9e-16	98-16		9e-16		96-16		7.5e-06			
END		158	160	107	107		108	108		108		108		901			
STAR T AA		2	2	50	49		8/	78	!	78		78		54			
CHAI N ID		¥	4		¥									T			
809 E1		9wga	9wga	1bx7	1du3		lmhu	Imhu		Imrt		Imr		1xka			
SEQ No B		1822	1822	1824	1824		1824	1824		1824		1824		1824			

PDB annotation			CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM- BINDING PROTEIN	CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM- BINDING PROTEIN	TRANSCRIPTION REGULATION PROTO-ONCOGENE, NUCLEAR BODIES (PODS), LEUKEMIA, 2 TRANSCRIPTION REGULATION	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS	HYDROLASE CPLA2; PHOSPHOLPASE, LIPID-BINDING, HYDROLASE	HYDROLASE CPLA2; PHOSPHOLIPASE, LIPID-BINDING,
Coumpound	METALLOTHIONEIN METALLOTHIONEIN ISOFORM II 4MT2 3	METALLOTHIONEIN METALLOTHIONEIN ISOFORM II 4MT2.3	PROTEIN KINASE C (BETA); CHAIN: A, B;	PROTEIN KINASE C (BETA); CHAIN: A, B;	TRANSCRIPTION FACTOR PML; CHAIN: NULL;	SYNAPTOTAGNIN I, CHAIN: A;	SYNAPTOTAGMIN I; CHAIN: A;	CYTOSOLIC PHOSPHOLIPASE A2; CHAIN: A, B;	CYTOSOLIC PHOSPHOLIPASE A2; CHAIN: A, B;
SEQFOL D score		127.57							
PMF	0.15		00.1	0.90	0.13	00:1	86'0	0.01	0.28
Verify score	-0.09		0.47	0.27	0.33	0.68	0.70	0.17	0.37
Psi Blast	1.3e-14	1.3e-14	4.8e-42	3.2e-37	0.00075	3.2e-46	1.46-27	1.1e-12	1.2e-15
AA	108	108	491	946	109	484	639	480	639
STAR	48	48	355	528	09	355	510	366	526
CHAI N ID			∢	Ą		<	¥	¥	٧
EDB CI	4mt2	4mt2	1a25	1a25	Ibor	Ibyn	Ibyn	lejy	lejy
SEQ NO.	1824	1824	1825	1825	1825	1825	1825	1825	1825

	-	_		_	_		_	_	_	_		_		_		_		_		-	_		_		_	7		_	-	_
PDB annotation	HYDROLASE	LIPID DEGRADATION PLC-DI; PHOSPHORIC DIESTER	HYDROLASE, HYDROLASE, LIPID	DEGRADATION, 2 TRANSDUCER,	CALCIUM-BINDING,	PHOSPHOLIPASE C, 3	PHOSPHOINOSITIDE-SPECIFIC	LIPID DEGRADATION PLC-D1;	LANDBOL ACT LINDBOL ACT 1 min	DEGRANATION 2 TRANSPICED	CALCIUM-BINDING.	PHOSPHOLIPASE C, 3	PHOSPHOINOSITIDE-SPECIFIC	LIPID DEGRADATION PLC-DI;	PHOSPHORIC DIESTER	HYDROLASE, HYDROLASE, LIPID	DEGRADATION, 2 TRANSDUCER,	CALCTUM-BINDING,	PHOSPHOLIPASE C, 3	PHOSPHOINOSITIDE-SPECIFIC	ENDOCYTOSIS/EXOCYTOSIS BETA	SANDWICH, CALCIUM ION, C2	ENDOCYTOSIS/FXOCYTOSIS BETA	SANDWICH CALCITIM ION C?	DOMAIN	TRANSFERASE CALCIUM++,	PHOSPHOLIPID BINDING PROTEIN,	CALCIUM-BINDING 2 PROTEIN,	PHOSPHATIDYLSERINE, PROTEIN	TRANSFERASE CALCIUM++,
Coumpound		PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A.	B,					PHOSPHOINOSITIDE-SPECIFIC	FROSE BOLLE ASE C, CHAIN: A,	ú				PHOSPHOINOSITIDE-SPECIFIC	PHOSPHOLIPASE C, CHAIN: A,	à.					SYNAPTOTAGMIN III; CHAIN:	A;	SYNAPTOTAGMIN III: CHAIN:	Α.	f.	PROTEIN KINASE C, ALPHA	TYPE; CHAIN: A;			PROTEIN KINASE C, ALPHA
SEQFOL D score																														
PMF		0.62						0.12						0.58							1.00		0.46			96'0				0.31
Verify		0.19						-0.07						91.0							0.47		0.24			0.33				0.38
Psi Blast		4.5e-15						6e-13						4.5e-15							3.2e-88		4.8e-33			1.3e-45				6.4c-40
END		467						970	_					467							649		129			494				650
STAR		370			_			526	_					370	_						357		512			354				510
CHAI N ID		<						٧						8							٧		A			¥				Ą
PDB ID		1djx						χģ						1djx							Idqv		Idav	-		Idsy	_			1dsy
SEQ No. ID		1825					-1	1825						1825				_		\neg	1825		1825			1825				1825

PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEQFOL	Coumpound	PDB annotation
	2	1 44	¥		score	score	D score		
								TYPE; CHAIN: A;	PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYLSERINE, PROTEIN KINASE C
	<	09	109	0.00045	0.10	0.10		CDK-ACTIVATING KINASE ASSEMBLY FACTOR MATI; CHAIN: A:	METAL BINDING PROTEIN RING FINGER PROTEIN MATI; RING FINGER (C3HC4)
		373	480	1.5e-16	-0.18	0.41		PHOSPHOLIPASE A2; CHAIN: NULL;	HYDROLASE CÁLB DOMÁIN; HYDROLASE, C2 DOMÁIN, CALB DOMÁIN
		528	631	7.5e-17	0.31	0.23		PHOSPHOLIPASE A2; CHAIN: NULL;	HYDROLASE CALB DOMAIN; HYDROLASE, C2 DOMAIN, CALB DOMAIN
		40	109	0.003	0,21	0.03		RAGI; CHAIN: NULL;	DNA-BINDING PROTEIN V(D)J RECOMBINATION ACTIVATING PROTEIN I; RAGI, V(D)J RECOMBINATION, ANTIBODY, MAD, RING FINGER, 2 ZINC BINGLIAGA CLUSTER, ZINC FINGER, DNA-BINDING PROTEIN
		347	483	4.8e-46			81.61	CALCIUMPHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	
		355	482	4.8e-46	0.81	1.00		CALCIUMPHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) 1RSY 3	
		510	636	1.6e-27	0.48	96'0		CALCIUMPHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) IRSY 3	
	٧	09	16	0.00075	0.04	0.16		PHOSPHATIDYLINOSITOL-3- PHOSPHATE BINDING FYVE	TRANSPORT PROTBIN FYVE DOMAIN, ENDOSOME

PDB annotation	MATURATION, INTRACELLULAR TRAFFICKING, 2 TRANSPORT PROTEIN	COMPLAS (GTP. BINDINGEFECTOR) RAS-RELATED PROTEIN RABSA, COMPLEX (GTP. BINDINGEFECTOR), O PROTEIN BEFECTOR, RABCHEL EXCYCTORIS, RAB PROTEIN, RABSA, RABPILLIN	COMPLEX (GTP. BINDINGEFFECTOR, RAS-RELATED ROTHIN RABBA; COMPLEX (GTP. BINDINGEFFECTOR, OR PROTEIN, EFFCTOR, RABCIR, 2 SYNAPTIC EXOCYTORSIS, RAB PROTEIN, RABA, RABPHLIN	ENDOCYTOSIS/EXOCYTOSIS C2-DOMAINS, C2B-DOMAIN, RABPHILIN, ENDOCYTOSIS/EXOCYTOSIS	ENDOCYTOSIS/EXOCYTOSIS C2-DOMAINS, C2B-DOMAIN, RABPHILIN, ENDOCYTOSIS/EXOCYTOSIS		CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
Coumpound	CHAIN: A;	RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	RABPHILIN 3-A; CHAIN: A;	RABPHILIN 3-A; CHAIN: A;	CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) ICLL 3	CALMODULIN; CHAIN: A; RS20; CHAIN: B;
SEQFOL D score			71.27			69.53	72.01
PMF		69.0		1.00	0.58		
Verify		0.40		0.62	0.53		
Psi Blast		3e-22	36-22	3.2e-29	1.4e-46	4.8e-53	1.10-60
END AA		120	131	496	649	691	170
STAR T AA		01	∞	357	512	29	56
CHAI N ID		Д	æ	V	<		4
80B 01		12bd	12bd	3rpb	3rpb	Icl	lvrk
SEQ Sign		1825	1825	1825	1825	1828	1828

PDB annotation	COMULEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHEOMBIN IIA, HYDROCHASE, SERINE PROTEINASE), PLASMA CALCUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD	COMPLEX (BLOOD COAGULATION/INHBITOR) AUTOPROTRICO/ABIN IIA, HYDROLASE, SERINE PROTEINASE, PLASMA CALCUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD	BLOOD COAGULATION, SERINE PROTRESS, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INTIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTRASE/CORACTORLIGAND)	BLOOD COAGULATION, SERINE PROTRASE, COMPLEX, CO-FACTOR, 2 RECEPTOR BAZYME, INHIBITOR, GLA, FGF, 3 COMPLEX (SERINE PROTRASE/COFACTOR/LIGAND)	HYDROLASE/HYDROLASE INHBITOR PROTEIN-PEPTIDE COMPLEX
Coumpound	ACTIVATED PROTEN C, CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	ACITYATED PROTEN C, CHAIN: C, I.; D-PHE-PRO-MAI; CHAIN: P;	BLOOD COAGULATION FACTOR VIIA; CHRIS: L, H; SOLUBLE TISSUE FACTOR; CHAIN; T, U; D-PHE-PHE-ARG- CHLOROMETHYLKETONE OPFERCMK, WITH CHAIN; C;	BLOOD COAGULATION FACTOR VUIA, CHARICI, H; SOLUBLE TISSUE FACTOR; CHAIN; T, U; D-PHE-PHE-ARG- CHAIN; T, U; THTH CHAIN; C;	DES-GIA FACTOR VIIA (HEAVY CHAN); CHAIN: H, I; DES-GIA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)- PHE-ARG CHAIN: C, D; PEPTIDE E-76: CHAIN: X, Y;
SEQFOL D score	58.73			60.57	
PMF		-0.17	0.96		0.99
Verify		0.14	0.10		0.26
Psi Blast	1.3e-20	1.3e-20	6.4e-16	1.5e-22	6.4e-16
END	145	202	231	193	231
STAR	47	73	152	75	152
CHAI N ID	1	1	ı	L)	1
EDB ID	Iaut	laut	Idan	Idan	1dva
SEQ NO:	1833	1833	1833	1833	1833

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PDB annotation	MATRIX PROTEIN EXTRACELULAR MATRDX, CALCIMABINDING, GLYCOROTEIN, SPEPAT, SIGNAL, MULTIGENE EAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMARN, HUMAN TERRILLIN-1 PERAGMENT, MATRIX PROTEIN	SIGNALLING PROTEIN BINDING PROTEIN, CYTOKINE, SIGNALLING PROTEIN	BLOOD CLOTTING COMPLEX(SERINE	PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE	PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR.	GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND),	BLOOD CLOTTING	GLYCOPROTEIN GLYCOPROTEIN	GLYCOPROTEIN GLYCOPROTEIN	COMPLEX (BLOOD	COAGULATION/INHIBITOR) CHRISTMAS FACTOR: COMPLEX	INHIBITOR, HEMOPHILIA/EGF,	BLOOD COAGULATION, 2 PLASMA,	SERINE PROTEASE, CALCIUM-	GLYCOPROTEIN	COMPLEX (BLOOD	COAGULATION/INHIBITOR) CHRISTMAS FACTOR: COMPLEX.
Coumpound	FIBRILLN; CHAIN: NULL;	TUMOR NECROSIS FACTOR RECEPTOR; CHAIN: A, B;	BLOOD COAGULATION FACTOR VIIA; CHAIN: L;	BLOOD COAGULATION FACTOR VIIA; CHAIN: H;	SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: 1;		1 AMININI CHAINI MIII 1 -	LAMININ: CHAIN: NULL:	LAMININ; CHAIN; NULL;	FACTOR IXA; CHAIN: C, L,; D-	PHE-PRO-ARG; CHAIN: I;					FACTOR IXA; CHAIN: C, L,; D-	PHE-PRO-ARG; CHAIN: I;
SEQFOL D score	56.72	54,06							70.82	64.61							
PMF			1.00				0.42	0.01								-0.12	
Verify			0.44				0.30	0.12								0.10	
Psi Blast	1.3e-15	9e-14	6.4e-16				10.08	1.1e-20	le-28	6e-35						6e-35	
END	226	173	231				200	242	247	146						218	
STAR T AA	149	10	152				43	56	95	22						54	
CHAI		∢	7							Т						T	
PDB ID	lemn	lext	1 fak				155	1klo	1klo	1pfx						1pfx	
SEQ NO:	1833	1833	1833				1833	1833	1833	1833						1833	

PDB annotation	INHIBITOR, HEMOPHILIA/EGF, BLOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM- BINDING, HYDROLASE, 3 GLYCOPROTEIN	COMPLEX (BLOOD) COAGULATION/INHIBITOR) COAGULATION/INHIBITOR) CHRISTINAS PACTOR, COMPLEX, INHIBITOR, HEMOEPHILABEGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCINH- BRUNDE, HYDROLASE, 3	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGUI-ATION, SERINE PROTEASE	SERINE PROTEASE FVIIA; PVIIA; BLOOD COAGULATION, SERINE PROTEASE
Coumpound		FACTOR IXA; CHAIN: C, L., D- PHE-PRO-ARG; CHAIN: I,	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION PACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYI. INHIBITOR; CHAIN: C.	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: 1; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPETIDYI, INHIBITOR; CHAIN: C;	COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION PACTOR VIIA
SEQFOL D score					55.94	
PMF		0.07	0.62	86:0		0.18
Verify		-0.16	0.07	0.30		90:04
Psi Blast		6c-29	1.5e-21	6.4e-15	7.5e-24	7.5e-24
END		226	226	231	561	207
STAR T AA		25	156	156	91	76
CHAI		1	L)	T	1	Т
rob CO		lpfx	1qfk	lqfk	1qfk	1qfk
SEQ NO: D		1833	1833	1833	1833	1833

PDB annotation		PLASMINOGEN ACTIVATION	PLASMINOGEN ACTIVATION	PLASMINOGEN ACTIVATION	LIPID DEGRADATION PHOSPHOLIPASE A2, LIPID DEGRADATION, HYDROLASE	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERNE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN	
Coumpound	(HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	T-PLASMINOGEN ACTIVATOR F1-G; 1TPG 7 CHAIN: NULL; 1TPG 8	T-PLASMINOGEN ACTIVATOR F1-G; 1TPG 7 CHAIN: NULL; 1TPG 8	T-PLASMINOGEN ACTIVATOR F1-G; ITPG 7 CHAIN: NULL; ITPG 8	PHOSPHOLIPASE A2; CHAIN: A, B;	BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR XA; CHAIN: I., C;	BLÖÖD COAGULATION FACTOR XA; CHAIN: L, C;	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3
SEQFOL D score							59.27		78.80
PMF		0.63	0.19	0.16	-0.12	0.64		90:0	
Verify		-0.02	0.27	0.23	0.03	0.18		0.32	
Psi Blast		Ie-23	le-23	30-21	4.5e-18	3e-18	1.16-21	1.16-21	7.5e-25
END		226	125	196	130	226	208	207	207
STAR T AA		137	43	72	34	156	16	36	28
CHAI N ID					٧	J	T	T	4
PDB TD		Itpg	Itpg	Itpg	Ivap	lvka	lxka	Ixka	9wga
SEQ ID NO:		1833	1833	1833	1833	1833	1833	1833	1833

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PDB annotation	SIGNALING PROTEIN PHOTOBECEPTOR, G PROTEIN- COUPLED RECEPTOR, MEMBRANE PROTEIN, 2 RETINAL PROTEIN, VISUAL PIGMENT	SIGNALING PROTEIN PHOTOREGEPTOR, O PROTEIN- COUTED RECEPTOR, MEMBRANE PROTEIN, 2 RETINAL PROTEIN, VISUAL PIGMENT		KNA-BINDING PROTEINKNA TRA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX	TRANKERASE TYPE II DNA- (CYTOSINE NA) METHYLITRANKERASE, AMINO 2 METHYLITRON SELENOMETHIONINE, MULTIWA VEILENOTH ANOMALOUS 3 DIRECTATION	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1, RRM, PROTEIN-RNA, COMPLEX, GENE REGULATION/RNA	GENE REGULATIONRNA POLY(A) BYDDNG PROTEIN, 1, PABP 1; RRM, PROTEIN-RNA, COMPLEX, GENE REGULATIONRNA
Coumpound	RHODOPSIN; CHAIN: A, B	RHODOPSIN, CHAIN: A, B	OUT I DITTAL DECEMBER OF A PRINCE	SAL-LE IHAL PROTEIN; CFAIN: A. B. RNA (5'- R(P*GP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP	N-4 CYTOSINE-SPECIFIC METHYLTRANSFERASE PVU II; CHAIN: A;	POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H, RIAA, (5- R(*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP*AP*AP*	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP* AP*AP*AP*AP*AP* AP*AP*AP*AP*AP* AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*A
SEQFOL D score							
PMF	-0.07	0.10	200	9770	0.27	0.24	-0.19
Verify score	0.11	-0.14	0.00	60:03	-0.57	-0.34	0.05
Psi Blast	3e-20	7.5e-18	1 60 10	61-50-1	4.5e-05	6.4e-23	3.2e-26
END	320	299	144	ŧ	480	150	237
STAR T AA	4	4	19	ē	433	29	22
CHAI N ID	<	В		<	∢	∢	æ
FDB ID	8841	881	11,76	1,01	1boo	lev]	lovj
SEQ NO DEQ	1834	1834	1025	3	1835	1835	1835

SEO	PDB	CHAI	STAR	END	Psi Blast	Verify	PMF	SEOFOL	Coumpound	PDB annotation
ВŞ	А	NID	TAA	ΑA	,	score	score	D score	•	
1835	ld2h	٧	424	492	1.2e-14	-0.57	0.17		GLYCINE N- METHYLTRANSFERASE; CHAIN: A, B, C, D;	TRANSFERASE METHYLTRANSFERASE
1835	1d9a	¥	72	144	3.2e-17	-0.02	91.0		HU ANTIGEN C; CHAIN: A;	RNA BINDING PROTEIN RNA- BINDING DOMAIN
1835	Idus	¥	421	292	9,6e-20	0.37	0.75		MJ0882; CHAIN: A;	STRUCTURAL GENOMICS HYPOTHETICAL PROTEIN, METHANOCOCCUS JANNASCHII
1835	ltje	¥	73	139	1.3e-13	0.19	0.62		NUCLEOLIN RBD2; CHAIN: A;	STRUCTURAL PROTEIN PROTEIN C23; RNP, RBD, RRM, RNA BINDING DOMAIN, NUCLEOLUS
1835	1g6q	1	402	280	3.2e-11	-0.51	0.03		HNRNP ARGININE N- METHYLTRANSFERASE; CHAIN: 1, 2, 3, 4, 5, 6;	TRANSFERASE SAM-BINDING DOMAIN, BETA-BARREL, MIXED ALPHA-BETA, HEXAMER, 2 DIMER
1835	1869	_	420	492	1.3e-13	0.20	0.83		HNRNP ARGININE N- METHYLTRANSFERASE; CHAIN: 1, 2, 3, 4, 5, 6;	TRANSFERASE SAM-BINDING DOMAIN, BETA-BARREL, MIXED ALPHA-BETA, HEXAMER, 2 DIMER
1835	1hd1	٧	74	144	3.2e-23	0.27	90:0		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN DO; CHAIN: A;	RNA BINDING PROTEIN RNA- BINDING DOMAIN
1835	Iqam	¥	410	592	6e-21	-0.06	0.58		ERMC' METHYLTRANSFERASE; CHAIN: A;	TRANSFERASE RRNA METHYLTRANSFERASE BRMC; COFACTOR ANALOGS
1835	Iqam	٧	413	524	6.4e-05	-0.12	0.05		ERMC' METHYLTRANSFERASE; CHAIN: A;	TRANSFERASE RRNA METHYLTRANSFERASE ERMC', COFACTOR ANALOGS
1835	lvid		424	538	1.5e-15	0.23	0.66		CATECHOL O- METHYLTRANSFERASE; CHAIN: NULL;	TRANSFERASE (METHYLTRANSFERASE) COMT; TRANSFERASE, METHYLTRANSFERASE, METHYLTRANSFERASE, DEGRADATION
1835	lxva	4	426	492	1.5e-10	-0.47	50.0		GLYCINE N- METHYLTRANSFERASE;	METHYLTRANSFERASE GNMT, S- ADENOSYL-L-METHIONINE);

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PDB annotation	GLYCINE METHYLTRANSFERASE	RNA BINDING PROTEIN RNA- BINDING DOMAIN	RNA-BINDING DOMAIN RNA- BINDING DOMAIN, ALTERNATIVE SPLICING	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR,	IKANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION		GENE REGULATION POZ DOMANI, PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2 REPRESSOR, ZINC-FINGER PROTEIN, X-RAY	CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION					BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR,
Coumpound	CHAIN: A, B;	MUSASHII; CHAIN: A;	SEX-LETHAL PROTEIN; CHAIN: NULL;	SEX-LETHAL; CHAIN: A, B, C;		The state of the s	PROMYELOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;		OXIDOREDUCTASE(OXYGEN(A)) GALACTOSE OXIDASE (E.C.1.1.3.9) (PH 4.5) 1GOP 3	OXIDOREDUCTASE(OXYGEN(A)) GALACTOSE OXIDASE (F.C. 1.1.3.9) (PH.4.5) 1GOF 3	OXIDOREDUCTASE(OXYGEN((E.C.1.1.3.9) (PH 4.5) IGOF 3	BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H;
SEQFOL D score													
PMF score		0.00	0.35	-0.05		000	-0.05		0.34	0.13	0.07		-0.20
Verify		-0.04	0.04	0.10			0.37		-0.33	-0.42	-0.23		-0.00
Psi Blast		4.8c-18	80-18	80-18			3.26-16		1.6e-06	7.5e-13	1.5e-15		4.8c-10
END		144	152	137		į	2		202	450	372		370
STAR T AA		74	73	19			4		204	217	246		285
CHAI N ID		٧		4		-	∢						13
PDB CI		2mss	2sxl	3sxl			ongr		1gof	lgof	1gof		1dan
SEQ E E	:	1835	1835	1835		2001	1830		1836	1836	1836		1837

No. D N TO TAA AA AA Store Story Decompound PDB annotation No. D TAA AA AA Store Story Soluble Tissue Factore County						т	
PDB CHA STAR END Psi Blast Verify PMF SEQPOL	PDB annotation	2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGP, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COPACTOR/LIGAND)	HYDROLASE/HYDROLASE INHBITOR PROTEIN-PEPTIDE COMPLEX	HYDROLASE/HYDROLASE INHBITOR PROTEIN-PEPTIDE COMPLEX	HYDROIASEHYDROIASE INHIBITOR PROTEIN-PEPTIDE COMPLEX
PDB CIAA STAR END Pai Baat Verify PAIF	Commound	SOLUBLE TISSUB FACTOR; CHAIN: T, U; D-PHE-PHE-ARG- CHLOROMETHYLKETONE (DFFRCMK) WITH CHAIN: C;	BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHAIN: CHOROMETHYLKETONE DPFRCAKE) WITH CHAIN: C.	BLOOD COAGULATION FACTOR VIA, CHARIE, I, H; SOLUBLE TISSUE PACTOR; CHAIN: T, U; D-PHE-PHE-ARG- CHAIN: T, U; D-PHE-PHE-ARG- CHOROMETHITAKETONE DEPECMK) WITH CHAIN: C;	DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN; I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: I, M; (DPN)- PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN; H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)- PHE-ARG; CHAIN: C, D; PEPTINE E-76; CHAIN: X, Y;	DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN: H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)- PHE-ARG; CFAIN: C, D;
PDB CHAI STAR END Psi Blast Verify	SEQFOL D score						
PDB CHAI STAR END Pti Biast	PMF		-0.20	-0.20	-0.20	-0.19	-0.20
PDB CHAI STAR END D NID TAA AA	Verify		0.04	0.21	60:0	0.10	0.27
PDB CHAI STAR DB N D TAA TAA CHAIN L 350 CHAIN L 285 CHAIN L 361 CHAIN L 361 CHAIN L 361 CHAIN L 350 CHAIN L 350 CHAIN L 350 CHAIN C			1.1e-12	3.2e-08	4.8e-10	1.1e-12	3.2e-08
PDB CHAI D	END AA		449	583	370	449	583
In Idea Idea Idea Idea Idea Idea Idea Idea	STAR		361	530	285	361	230
PDB 10 10 10 10 10 10 10 10 10 10 10 10 10	CHAI N ID		ם	1	1	1	ı
	PDB TD						
	SEQ NO.		1837	1837	1837		1837

PDB annotation	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCUM-BINDING, GLYCOROTEIN, ERBEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMARN, HUMAN FIRELLIN-1 PRAGMEYT, MATRIX PROTEIN	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIMABINDING, GIVCOROFIENI, SEPERAT, SIGNAL, MUTTGENE PREBLIX, DISBABE MUTATION, 3 EGFLIKE DOMANN, FINDAN FEBRLLIN-1 FRAGMENT, MATRIX PROTEIN	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCILM-BINDING, GLYCORNOTEIN, 2 REPRAT, SIGNAL, MULTIGENE FAMILY, DISEASE MULTIGENE FAMILY, DISEASE MUTATION, 3 EGE-LIKE DOMANN, HUMAN PRELLIKI-1	LIPID BINDING PROTEIN LDL RECEPTOR; BETA HAIRPIN, 3-10 HELIX, CALCIJM BINDING	LIPID BINDING PROTEIN LDL RECEPTOR; BETA HAIRPIN, 3-10 HELIX, CALCIUM BINDING	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE
Coumpound	FIBRILLN; CHAIN: NULL;	FIBRILLIN; CHAIN: NULL;	FIBRILLIN; CHAIN: NULL;	LOW-DENSITY LIPOPROTEIN RECEPTOR; CHAIN: A;	LOW-DENSITY LIPOPROTEIN RECEPTOR; CHAIN: A;	BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H;
SEQFOL D score	,					
PMF	-0.19	-0.17	-0.20	-0.20	-0.20	-0.20
Verify score	0.19	0.07	0.03	0.03	0.13	0.22
Psi Blast	1.4e-10	3.2e-09	4.8e-09	1.6e-11	4.8c-09	3.2e-08
END	185	227	283	182	221	583
STAR T AA	107	149	530	102	143	530
CHAI				<	<	T
EDB TD	lemn	1emn	lemn	1f5y	Iffy	Ifak
SEQ NO:	1837	1837	1837	1837	1837	1837

PDB annotation	BLOOD COAGULATION, SERINE PROTEASE		BLOOD COAGULATION FACTOR STUART FACTOR, BLOOD COGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR, LIKE DOMAN	BLOOD COAGULATION FACTOR STUART FACTOR, BLOOD COAGULATION FACTOR, SERINE PROTEINASF, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN			HYDROLASE HYDROLASE, NAD BINDING PROTEIN	OXIDOREDICTASE OXIDOREDICTASE, TROPANE ALKALOID BIOSYNTHERSIS, REDICTION OF 2 TROPINONE TO TROPINE, SHORT-CHAIN
	PROTEASE		BLOOD STUAR COAGL PROTE GROW	BLOOD STUAR COAGU PROTE GROW			HYDRC	OXIDO OXIDO ALKAL REDUC TROPIN
Coumpound	(LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPPTIDYL INHIBITOR; CHAIN: C;	MEMBRANE PROTEIN VITELLINE MEMBRANE OUTER LAYER PROTEIN I IVMO 3	BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	S-ADENOSYLHOMOCYSTEINE HYDROLASE; CHAIN: A, B;	TROPINONE REDUCTASE-1; CHAIN: A, B;
SEQFOL D score								
PMF		-0.19	-0.20	-0.20	-0.14	-0.14	0.00	0.21
Verify score		0.19	0.22	0.04	0.21	0.01	-0.09	0.34
Psi Blast		3e-15	1.6e-08	4.8e-11	9.6e-16	4.8e-16	0.0032	0.00064
END		470	585	158	403	476	202	215
STAR		303	530	73	250	275	163	173
CHAI		Ą	L)	T	٧	∢	٧	∢
PDB ID		lvmo	1xka	lxka	9wga	9wga	la7a	laci
SEQ ID NO:		1837	1837	1837	1837	1837	1838	1838

PDB annotation	ALCOHOL DEHYDROGENASE 1DEH	OXIDOREDUCTASE BETAI ADH; IDEH 9 NAD+ DEPENDENT ALCOFOL DEHYDROGENASE IDEH 26	ALCOHOL DEHYDROGENASE ALCOHOL DEHYDROGENASE	OXIDOREDUCTASE DEHYDROGENASE, ALCOHOL, NICOTINAMIDE COENZYME, STEROID 2 BINDING		OXIDOREDUCTASE, ZINC, NADP	OXIDOREDUCTASE OXIDOREDUCTASE, ZINC, NADP	OXIDOREDUCTASE OXIDOREDUCTASE		
Coumpound	CHAIN: A, B; 1DEH 8	HUMAN BETAI ALCOHOL DEHYDROGENASB; IDEH 7 CHAIN: A, B; IDEH 8	ALCOHOL DEHYDROGENASE, CLASS II; CHAIN: A, B;	ALCOHOL DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE 3-ALPHA, 20-BETA-HYDROXYSTEROID DEHYDROGENASE (E.C.1.1.153) 1HDC 3 COMPLEXED WITH CARBENOXOLONE 1HDC 4	NADP-DEPENDENT ALCOHOL DEHYDROGENASE; CHAIN: A, B, C, D;	NADP-DEPENDENT ALCOHOL DEHYDROGENASE; CHAIN: A, B, C, D;	FLAVOCYTOCHROME C3 FUMARATE REDUCTASE; CHAIN: A, D;	OXIDOREDUCTASE QUINONE OXIDOREDUCTASE COMPLEXED WITH NADPH 1QOR 3	OXIDOREDUCTASE QUINONE OXIDOREDUCTASE COMPLEXED WITH NADPH
SEQFOL D score		74.95				53.09			116.09	
PMF			1.00	00'1	0.45		1.00	0.47		1.00
Verify score			0.77	0.73	-0.03		0.59	0.28		0.75
Psi Blast		3.2e-81	1.6e-69	4.8e-77	9.6e-07	1.6e-51	1.6e-51	0.0032	8e-70	8e-70
END		367	366	366	284	369	367	207	370	367
STAR		E.	26	22	173	24	20	891	37	38
CHAI		<	<	<	<	<	٧	٧	٧	٧
PDB CI		Ideh	le3i	lee2	Thde	Ikev	Ikev	Iqo8	Iqor	Iqor
SEQ NO:		1838	1838	1838	1838	1838	1838	1838	1838	1838

CHAI STAR NID TAA	TAA	⊤ ہے ا	END	Psi Blast	Verify	PMF	SEQFOL D score	Coumpound	PDB annotation
A 1 367	1 36	36	£	1,6e-86			72.11	OORS HUMAN CHICH ALCOHOL DBHYDROGBNASE; CHAIN: A, B;	OXIDOREDUCTASE GLUTATHONE- DREVENDENT PORMALDEHYDE DREFUNDENT ALCOHOL DRETUNDENT ALCOHOL DRETUNDENT ALCOHOL GLUTATHONE DEPENDENT FORMALDEHYDE PORMALDEHYDE
A 27 366		36	9	1.6e-86	09.00	1.00		HUMAN CHICH ALOOHOL DBHYDROGENASE, CHAIN: A, B;	OKIDOREDUCTASE GLITATIEIONE- DEPENDENT PORMALDEHYDE DEPENDENT PORMALDEHYDE DEPENDENT ALCOHOL DEHYDROGENASE 2 GLUTATHIONE DEPENDENT FORMALDEHYDE
164 268		582		60000	0.51	0.47		CATECHOL O- METHYL,TRANSFERASE; CHAIN; NULL;	TRANSBERASE (METHYLTRANSFERASE) COMT; TRANSFERASE, METHYLTRANSFERASE, NEUROTARANSMITTER DEGRADATION
A 173 280		280		9.6e-05	-0.20	0.49		TRIHYDROXYNAPHTHALENE REDUCTASE; CHAIN: A, B;	OXIDOREDUCTASE NAPHTHOL REDUCTASE, OXIDOREDUCTASE
		37	0	4.8e-54			52.30	NADP-DEPENDENT ALCOHOL DEHYDROGENASE; CHAIN: A, B, C, D;	OXIDOREDUCTASE OXIDOREDUCTASE
A 52		ř	367	4.8e-54	0.56	1.00		NADP-DEPENDENT ALCOHOL DEHYDROGENASE; CHAIN: A, B, C, D;	OXIDOREDUCTASE OXIDOREDUCTASE
71 34		£	349	9.6e-09			52.68	CALCIUM/CALMODULIN- DEPENDENT PROTEIN KINASE;	KINASE KINASE, SIGNAL TRANSDUCTION,

				_		,_	_		_	_			_		_	_	_	_		_	_				,-					_	_
CALCIUM/CALMODULIN	COMPLEX (ISOMERASE/PROTEIN KINASE) FKBP12;	SERINE/THREONINE-PROTEIN	KINASE RECEPTOR R4; COMPLEX	(ISOMERASE/PROTEIN KINASE),	RECEPTOR 2 SERINE/THREONINE KINASE	COMPLEX (ISOMERASE/PROTEIN	KINASE) FKBP12;	SERINE/THREONINE-PROTEIN	KINASE RECEPTOR R4; COMPLEX	(ISOMERASE/PROTEIN KINASE),	RECEPTOR 2 SERINE/THREONINE	KINASE	TRANSFERASE CSK; PROTEIN	KINASE, C-TERMINAL SRC KINASE,	PHOSPHORYLATION, 2	STAUROSPORINE, TRANSFERASE	TRANSFERASE CSK; PROTEIN	KINASE, C-TERMINAL SRC KINASE,	PHOSPHORYLATION, 2	STAUROSPORINE, TRANSFERASE	TRANSFERASE CSK; PROTEIN	KINASE, C-TERMINAL SRC KINASE,	PHOSPHORYLATION, 2	STAUROSPORINE, TRANSFERASE	PHOSPHOTRANSFERASE FGFR1K,	FIBROBLAST GROWTH FACTOR	RECEPTOR I; TRANSFERASE,	TYROSINE-PROTEIN KINASE, ATP-	BINDING, 2 PHOSPHOR YLATION,	RECEPTOR,	PHOSPHOTRANSFERASE
CHAIN: NULL;	FK506-BINDING PROTEIN; CHAIN: A, C, E, G; TGF-B	SUPERFAMILY RECEPTOR	TYPE I; CHAIN: B, D, F, H;			FK 506-BINDING PROTEIN;	CHAIN: A, C, B, G; TGF-B	SUPERFAMILY RECEPTOR	TYPE I; CHAIN: B, D, F, H;				C-TERMINAL SRC KINASE;	CHAIN: A;			C-TERMINAL SRC KINASE;	CHAIN: A;			C-TERMINAL SRC KINASE;	CHAIN: A;			_						
	58.79												62.45												70.22						
						90.0											00.0				0.01										
						-0.17											-0.33				-0.39										
	1.1e-15					1.5e-13							3.2e-27				1.5e-13				3.2e-27				1.1e-26						
	350					199							337				197				334				339						
	05					70							73				78				87				49						
	В					В							Ą				¥				₹				¥						_
	1b6c					1b6c							lbyg				lbyg				1byg				1fgk						
	1839					1839							1839				1839				_				1839						
		156c B 50 1.16-15 58.79 CHARN-NULL; CHARN-NULL; CHARN-NULL; CHARN-A, C, E, G, TGF-B	1566 B 50 350 1.1e-15	1566 B	1666 B 50 550 1.16-15	116-15 12-15 12-16 12-	1560 B 50 350 116-15 5879 CFARRY NOTE PROTEIN: CFARRY	1566 B 50 350 1.16-15 78.79 7CAARN: WING PROTEIN; 7CAARN: W.O.C. G., TGF-B; 7CAARN: G., G., G., TGF-B; 7CAARN: G., G., G., TGF-B; 7CAARN: G., G., G., G., G., G., TGF-B; 7CAARN: G.,	1860 B	1966 B 50 350 1.16-15 78.79 77.206.BINDING REOTEIN; 77.79 77	156c B 50 350 1.1e-15 58.79 FCSAGE-BINDING PROTEIN- CTANIN S. L. G. G. TICE-B- CTANIN S. C. G. G. TICE-B- CTANIN S. C. G. G. G. TICE-B- CTANIN S. C.	116-15 116-15 11736-1010/R POTEN, 11	1566 B 50 350 1.1e-15 58.79 FCSG-GRIDDING PROTEIN, CAPARIN, MILE &	1966 B 50 350 1.16-15 1.26-13 1.	10c B 50 350 1.1c-1.5 1.879 1.574 1.57	The base B S0 350 116-15 The base The bas	1566 B 50 350 1.16-15 1.879 1.74 AR SUPPLING REPORTED.N 1569 B 70 199 1.56-13 -0.17 0.06 1.70 1.50 B. D. F. H. 1560 B 70 199 1.56-13 -0.17 0.06 1.50 B. D. F. H. 1561 B 70 199 1.56-13 -0.17 0.06 1.50 B. D. F. H. 1562 B 70 73 73 73 73 73 74 74 74	Dec B S0 350 1.16-15 S3.79 PCM-RN-WING PROTEIN, CAPARIS-WING PROTEIN, CAPARIS-MIN-RESERVOR. PCSG-BINDING PROTEIN, CAPARIS-MIN-RESERVOR. PCSG-B	156 B 50 350 1.16-15 1.25	The S S S S S S S S S	1966 B 50 350 1.16-15 1.879 CFARR-WIND ROTEIN. 1966 B 70 199 1.56-13 -0.17 0.06 CFARR-MILY RECEPTOR 1967 A 73 33-7 3.26-27 CFARR-MILAL SRC KINASE; 1968 A 78 197 1.56-13 -0.33 0.00 CFTRMINAL SRC KINASE; 1969 A 73 33-27 0.245 CFTRMINAL SRC KINASE; 1969 A 78 197 1.56-13 -0.33 0.00 CFTRMINAL SRC KINASE; 1960 CFTRMINAL SRC KINASE;	1966 B 50 350 116-15 15.00 116-15 15.00 116-15 15.00 116-15 15.00 116-15 15.00 1	1966 B 50 350 1.16-15 1.879 CFARRYUND REOTEIN 1966 B 70 199 1.56-13 -0.17 0.06 CFARRYUND REOTEIN 1967 A 73 337 3.26-27 0.245 CFRAINAL SEC KINASE; 1968 A 78 197 1.56-13 -0.33 0.00 CFRAINAL SEC KINASE; 1969 A 78 73 3.26-27 0.245 CFRAINAL SEC KINASE; 1969 A 78 78 78 78 78 78 78	Dec B S0 350 1.1e-15 R.S. P.S. P.S.	1966 B 50 350 1.16-15 1.879 CFARRYUND REOTEIN. 1966 B 70 199 1.56-13 -0.17 0.06 CFARRYUND REOTEIN. 1967 A 73 337 3.26-27 0.245 CFRAINAL SRC KINASE; 1968 A 78 197 1.56-13 -0.33 0.00 CFRAINAL SRC KINASE; 1969 A 78 73 3.26-27 0.245 CFRAINAL SRC KINASE; 1969 A 78 78 78 78 78 78 78	The base B S0 350 11e-15 The base The bas	1966 B 50 350 1.16-15 1.26-13 1.	Dec B S0 350 11e-15 S3.79 CFARRY MINAL SRC KINASE; CFARRY	1966 B 50 350 1.16-15 1.26-13 1.	The S S S S S S S S S	1966 B 50 350 1.16-15 1.54 1.54 1.54 1.56 1.16-15 1.57 1.56 1.16-15 1.57 1.56 1.16-15 1.57 1.56 1

PDB annotation	PHOSPHOTRANSFERASE FGFRIK, FIBROBLAST GRWYHI FACTOR RECEPTOR I; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP- BINDING, 2 PHOSPHORYLATION, RECEPTOR,	PHOSPHOTRANSFERASE FGFRIK, FIBRODA-AST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP- BINDING, 2 PHOSPHORYLATION, RECEPTOR,	TRANSFERASE P150, C-ABL; KINASE, KINASE INHIBITOR, STI- 571, ACTIVATION LOOP	PROTEIN KINASE CDK2; TRANSFBRASE, SERNIE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION	COMPLEX CRANSPERASE SUBSTRATE) TYROSINE KINASE, SIGNAL MASSIDICTION PHOSPHOTIVANNERASE, 2 SOMELEX (KINASE/PETIDE SUBSTRATIBATIP ANALOG), SUBSTRATIBATIP ANALOG), TRANSPERASE SUBSTRATES (TRANSPERASE)	COMPLEX (TRANSFERASE/SUBSTRATE)
Commound	FGF RECEPTOR 1; CHAIN: A, B;	FGF RECEPTOR I; CHAIN: A, B;	PROTO-ONCOGENE TYROSINE-PROTEIN KINASE ABL; CHAIN: A, B;	HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	INSULIN RECEPTOR; CHAIN: A; B;	INSULIN RECEPTOR; CHAIN: A; PEPTIDE SUBSTRATE; CHAIN:
SEQFOL D score	71.37				61.82	
PMF		0.41	0.10	0.33		0.16
Verify score		0.11	-0.20	-0.13		0.10
Psi Blast	3.26-26	3.2e-26	1.6e-27	1.4e-22	3.26-26	3.2e-26
END	338	335	332	321	350	332
STAR T AA	8	48	84	7.9	8	87
CHAI N ID	m	æ	٧		∢	A
PDB ED	Ifgk	1fgk	1fpu	Ihoi	Eil Eil	1ir3
SEQ No.	1839	1839	1839	1839	1839	1839

PDB annotation	TYROSONE KINASE, SIGNAL TRANSDUCTION. PHOSPHOTRANSFERASE, 2 COMPLEX (KINASSPERTIDE SUBSTRATEATE ANALOG). ENTYME, 3 COMPLEX (TRANSFERASE/SUBSTRATE)	TYROSINE KINASE TYROSINE KINASE-INHIBITOR COMPLEX, DOWN-REGULATED KINASE, 2 OKDERED ACTIVATION LOOP	TRANSFERASE KDR; TYROSINE KINASE	CONTRACTILE PROTEIN TROPOMYOSIN COLLED-COLL ALPHA-HELICAL, CONTRACTILE PROTEIN	ISOMERASE ISOMERASE, MUTASE, INTRAMOLECULAR TRANSFERASE	ORAPE EX (TRANSDUCETION) OT BETA-CHAMACA, MEKA, PERS, BETA-CHAMACA, AREA, PERS, GAMAA, SIGNAL TRANSDUCTION, PEGULATION, PHOSEDOMN, 3 VISION, G PROTEINS, COMPLEX CONTRANSDUCTION, COMPLEX CONTRANSDUCTION) (TRANSDUCERNITANNSDUCTION)	COMPLEX (ZINC FINGER/DNA),
Coumpound	Ŕ	HAEMATOPOETIC CELL KINASE (HCK); CHAIN: A;	VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR CHAIN: A;	TROPOMYOSIN; CHAIN: A, B, C, D	METHYLMALONYL-COA MUTASE; CHAIN: A, B, C, D;	TRANSDUCIN; CHAIN: B, G; PHOSDUCIN; CHAIN: P;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX
SEQFOL D score							
PMF		0.29	0.03	-0.20	-0.13	-0.19	00:00
Verify score		-0.26	-0.38	0.14	0.19	0.53	-0.46
Psi Blast		1.1e-24	1.6e-20	8e-09	1.3e-08	4.5e-09	8e-23
END		347	336	176	164	112	161
STAR T AA		84	87	5	2	9	117
CHAI N ID		V	A	V	<	A.	Ą
PDB		1qcf	lvr2	lelg	Ireq	2trc	lalh
SEQ NO E		1839	1839	1840	1840	1840	1841

PDB annotation	ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTFIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN		COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL, STRUCTURE, COMPLEX
Coumpound	OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE: CHAIN: B. C.	QGSR ZINCFINGS; QGSR ZINCFINGS; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE: CHAIN: B. C:	QGSR ZINC FINGER PEPTIDE; CHAN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE: CHAIN: B. C:	QOSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE: CHAIN: B. C:	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B. C;	TRANSCRIPTION RECULATION TAGAST TRANSCRIPTION FACTOR ADRI (RESIDUES 102- 103 IARD 3 (AMINO TERMINAL ZINC PROGRE DOMAIN) (AMR. 10 DOMAIN) (AMR. 10 TREMINES) 1ARD 4 (ADRIB) ARD 5 IARD 5 IARD 5 IARD 6 IARD 6 IARD 7 IARD 7	DNA; CHAÎN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAÎN: C, F, G;
SEQFOL D score		75.37						
PMF			0.93	0.25	0.33	0.87	0.81	0.22
Verify score			97.18	90:00	-0.34	-0.66	-0.12	-0.12
Psi Blast		6.4e-30	6.4e-30	3.2e-26	6.4e-24	6.4e-30	1.6c-06	I.6e-38
END		249	247	281	400	428	376	191
STAR T AA		166	167	195	325	348	348	109
CHAI N ID		<	A	₹.	<	V		၁
EDB EDB		lalh	laih	lalh	lalh	lalh	lard	Imey
SEQ ID NO:		1841	1841	1841	1841	1841	1841	1841

SEQ No u	PDB U	CHAI	STAR T AA	END AA	Psi Blast	Verify	PMF	SEQFOL D score	Coumpound	PDB annotation
										(ZINC FINGER/DNA)
1841	1тсу	c	138	219	1.6e-47	-0.01	86.0		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC BENGED DE CTEIN DNA
									PROTEIN: CHAIN: C. F. G.	INTERACTION, PROTEIN DESIGN, 2
										CRYSTAL STRUCTURE, COMPLEX
										(ZINC FINGER/DNA)
1841	Imey	C	166	247	1.6e-48	0.11	1.00		DNA; CHAIN: A, B, D, B;	COMPLEX (ZINC FINGER/DNA) ZINC
									CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
										CRYSTAL STRUCTURE, COMPLEX
										(ZINC FINGER/DNA)
1841	Imey	ပ	166	248	1.6e-48			83.84	DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
									CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
										CRYSTAL STRUCTURE, COMPLEX
										(ZINC PINGER/DNA)
1841	lmey	ပ	194	282	8e-45	-0.14	0.22		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
									CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
										CRYSTAL STRUCTURE, COMPLEX
										(ZINC FINGER/DNA)
1841	lmey	ပ	324	400	1.1e-41	-0.60	0.22		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
									CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
										CRYSTAL STRUCTURE, COMPLEX
										(ZINC FINGER/DNA)
1841	Imey	ပ	347	428	1.6e-45	-0.19	0.82		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
									CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
										CRYSTAL STRUCTURE, COMPLEX
										(ZINC FINGER/DNA)
1841	Imey	ŋ	220	247	I.le-12	0.13	0.70		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
									CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2

	PDB ID	CHA1 N ID	STAR T AA	END AA	Psi Blast	Verify	PMF	SEQFOL D score	Coumpound	PDB annotation
										CRYSTAL STRUCTURB, COMPLEX (ZINC FINGER/DNA)
	lmey	O	345	372	6.4e-13	-0.26	0.95		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA
									PROTEIN; CHAIN: C, F, G;	INTERACTION, PROTEIN DESIGN, 2
										CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
_	1mey	G	401	428	1.6e-13	0.03	0.48		DNA; CHAIN: A, B, D, E;	COMPLEX (ZINC FINGER/DNA) ZINC
									CONSENSUS ZINC FINGER	FINGER, PROTEIN-DNA
									5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	CRYSTAL STRUCTURE, COMPLEX
										(ZINC FINGER/DNA)
_	1sp2		348	376	8e-09	-0.21	0.03		SP1F2; CHAIN: NULL;	ZINC FINGER TRANSCRIPTION
										FACTOR SP1; ZINC FINGER, TRANSCRIPTION ACTIVATION, SP1
_	1163	٧	195	267	I.1e-20	0.03	-0.11		TRANSCRIPTION FACTOR IIIA;	COMPLEX (TRANSCRIPTION
									CHAIN: A; 5S RNA GENE;	REGULATION/DNA) TFIIIA; 5S
									CHAIN: E, F;	GENE, NIMK, IFIIIA, PROTEIN, DNA,
										GENE. DNA BINDING PROTEIN.
										ZINC FINGER, COMPLEX 3
										(TRANSCRIPTION
1	911	4	112	278	3.2e-33			74.20	TEIIIA: CHAIN: A. D: 5S	COMPLEX (TRANSCRIPTION
	_			ì					RIBOSOMAL RNA GENE;	REGULATION/DNA) COMPLEX
									CHAIN: B, C, E, F;	(TRANSCRIPTION
										REGULATION/DNA), RNA
	_									POLYMERASE III, 2
	_									TRANSCRIPTION INITIATION, ZINC
1-	1+66	4	130	284	3 20.33	26.0	0 0		Tellia, Cuani, a P. se	COAMI EV CO AMECUATION
	_	:	}	-		}	}		RIBOSOMAL RNA GENE;	REGULATION/DNA) COMPLEX
									CHAIN: B, C, E, F;	(TRANSCRIPTION
4	1			1	1	1				REGULATION DINAJ, KINA

PDB annotation	POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX	(TRANSCRIPTION PROPERTY PROPERTY ATTOMICANO)	POLYMERASE III, 2	TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCRIPTION	REGULATION/DNA) COMPLEX	REGIL ATTOMONA), RNA	POLYMERASE III, 2	TRANSCRIPTION INITIATION, ZINC	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-YANG 1;	TRANSCRIPTION INITIATION,	INITIATOR ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-PROTEIN	RECOGNITION, 3 COMPLEX	(TRANSCRIPTION	COMMISS (TRI ANGORITHM)	PECIFICACIONES CALLEDON	KEGULAHUN/DINA) YING-YANG I;	DIMANSCRIPTION INITIATION,	INITIATOR ELEMENT, Y Y1, ZINC 2	PECOCATTION 2 COLUMN	AECOGNITION, 3 COMPLEX	REGIL ATTONONA)	COMPLEX (TRANSCRIPTION
Coumpound		TFIIIA; CHAIN: A, D; 5S RIBOSOMAI, RNA GENE;	CHAIN: B, C, E, F;			TFIIIA; CHAIN: A, D; 5S	RIBOSOMAL RNA GENE;	CHAIN: B, C, E, F;			YYI; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;				VOCI, CITATNI, C. ADENIO	111, CIPAIN, C, ADDING.	Associated vikus pa	CHARL & B.	CHAIN: A, B;				YY1; CHAIN: C; ADENO-
SEQFOL D score																		. 20 02	1011							
PMF		0.19				0.04					0.19															0.78
Verify		-0.30				-0.37					-0.16															-0.33
Psi Blast		4.8e-31				6.4e-34					3.2e-30						_	20.23	25-25							3e-32
END		437				488					219							3.40	240							247
STAR		297				348					601							140	3							143
CHAI N ID		Ą				A					o							L	,							O
PDB		1476				1166					lubd							1.mpd	3							lubd
SEQ ID NO:		1841				1841					1841							1841	1							1841

	1			r — —		1
PDB annotation	REGULATIONDNA) YING-YANG I; TRANSCRIPTON METHATION, INITATOR ELEMENT, YY, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION) RECULATIONDAN)	COMPLEX (TRANSCRIPTION REGULATION/DINA) YNG-Y-NG I; TRANSCRIPTON INTIA/TON, INTIA/TOR ELEMBRT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION) REGULATION/DNA)	COMPIEX (TRANSCRIPTION REGULATIONDNA) YNG-YNG 1; TRANSCRIPTON INTIATION, INTTAOR ELEMENT, YY1, ZINC 2 FINGER REOTERN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION)		COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING
Coumpound	ASSOCIATED VIRUS PS INITIATOR ELEMENT DIVA; CHAIN: A, B;	VYI; CRAIN: C, ADBNO. ASSOCIATBO VIRUS PS. INITIATOR BEIGHBYT DNA; CHAIN: A, B;	VYI; CIAIN: C, ADBNO- ASSOCIATED VIRUS PS INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX(TRANSCRIPTION REGULATION/DNA) TRAMTRACK PROTEIN (TWO ZINC-FINGER PEPTIDE) COMPLEXED WITH 2DRP 3 DNA 2DRP 4	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII;
SEQFOL D score					76.50	
PMF		0.04	0.40	0.01		0.62
Verify score		-0.25	-0.46	-0.52		-0.12
Psi Blast		3.2e-32	6.46-30	4.8c-06	1.6e-32	6e-29
END		281	428	371	283	252
STAR T AA		174	332	323	138	140
CHAI N ID		U	o o	٧	<	Ą
EDB CI		lubd	1ubd	2drp	2gli	2gli
SEQ NO:		1841	1841	1841	1841	1841

Coumpound PDB annotation	; CHAIN: C, D; PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	ROTEIN CLII; COMPLEX (DNA-BINDING ; CHAIN: C, D; PROTEININA), PIYE-FINGER GII; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	IN; CHAIN: A, STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN ALPHA	HELICAL LINKER REGION, 2.2	TANDEM 3-HELIX COILED-COILS, STRUCTURAL PROTEIN	-	REPEATS OF SPECTRIN, ALPHA HELICAL LINKER PEGION 22	TANDEM 3-HELIX COILED-COILS,	STRUCTURAL PROTEIN	DING PROTEIN ENDOCYTOSIS/EXOCYTOSIS		-	Z		-	-	_	COMPLEX, MULTI-SUBUNIT	SYNTAXIN-1A; CHAIN: A, B, C; ENDOCYTOSIS/EXOCYTOSIS	SYNAPTOTAGMIN ASSOCIATED 35	KDA PROTEIN, P35A, THREE HELIX	BUNDLE	SYNTAXIN-14; CHAIN: A, B, C; ENDOCYTOSIS/EXOCYTOSIS SYNTAXIN-14; CHAIN: A, B, C; ENDOCYTOSIS/EXOCATED 35
	CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ALPHA SPECTRIN; CHAIN: A, B. C:	ī		ALPHA SPECTRIN; CHAIN: A,	В, С;			SYNTAXIN BINDING PROTEIN	1; CHAIN: A; SYNTAXIN 1A;	CHAIN: B;	SYNTAXIN BINDING PROTEIN	1; CHAIN: A; SYNTAXIN 1A;	CHAIN: B;	SYNTAXIN BINDING PROTEIN	1; CHAIN: A; SYNTAXIN 1A;	CHAIN: B;	SYNTAXIN-1A;				SYNTAXIN-1A;
SEQFOL D score																							
PMF		-0.05	-0.17			000				-0.20			-0.20			-0.17			-0.19				-0.19
Verify		60.00	1.09			0.39				0.41			0.57			0.43			0.78				0.83
Psi Blast		1.6e-32	1.5e-09			7.5e-05				4,5e-10			1.5e-17			1.5e-11			1e-09				3e-16
END		283	848			862				613			642			769			376				109
STAR T AA		146	511			999				437			481			513			447				482
CHAI		4	¥			<				Д			В			ф			∢				∢
10 B		2gli	Icun			1cm				ldnl			IdpI			Idni			lez3				lez3
SEQ NO:		1841	1845			1845				1845			1845			1845			1845				1845

PDB annotation	BUNDLE	B, C; ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE	B, C; ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE	B, C; ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN ASSOCIATED 35 KDA PROTEIN, P35A, THREE HELIX BUNDLE	SIGNALING PROTEIN GBP, GTP HYDROLYSIS, GDP, GMP, INTERPERON INDICED, DYNAMIN 2 RELATED, LARGE GTPASE FAMILY, GMPPNF, GPPNFP,		T	ISOMERASE ISOMERASE, MUTASE, INTRAMOLECULAR TRANSFERASE	3		TOTAL CONTRACTOR
Coumpound		SYNTAXIN-1A; CHAIN: A, B, C;	SYNTAXIN-1A; CHAIN: A, B, C;	SYNTAXIN-1A; CHAIN: A, B, C;	INTERFERON-INDUCED GUANYLATB-BINDING PROTEIN I; CHAIN: A;	SSO1 PROTEIN; CHAIN: A;	HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	METHYLMALONYL-COA MUTASE; CHAIN: A, B, C, D;	RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;	RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;	
SEQFOL D score											
PMF		-0.20	-0.17	0.00	-0.19	-0.20	-0.19	-0.08	0.15	-0.20	
Verify score		Ξ	86'0	0.21	0.74	0.55	0.70	0.48	0.76	0.40	
Psi Blast		1.5e-16	3e-I6	4.5e-05	3e-08	9e-13	3e-24	4.5e-31	4.5e-18	6e-17	
END		630	828	861	929	642	929	746	643	21.9	
STAR		511	526	739	485	485	460	451	485	486	
CHAI N ID		∢	٧	<	V	A	¥	A			
PDB		lez3	lez3	lez3	1f3n	Ifio	Iduu	lreq	Isig	Isig	
SEQ El Si		1845	1845	1845	1845	1845	1845	1845	1845	1845	

PDB annotation	TRANSDICENTONS TOTAL STATES THOSDUCIN, TRANSDICTION TRANSDICTIN, BETA- GAMMA, SIGNAL,	COMPLEX CONDERFORMANCE (TRANSDUCTION) CHERY-CANAMAR MERGA, PESS; PHOSDICORY, TRANSDUCTION, 2 REGULATION, 2 REGULATION, 2 REGULATION, CONDERFORMARION, STOOMBON, THIOREDORY, 3 VISION, MERCA, CONDERFORMARION, CONDERFORMARION	COMPLEX (TRANSDUCER/TRANSDUCTION) OF BEILA-GAMMA, MERA, 1973; BEILA-GAMMA, RESTA, 1973; GAMMA, SIGNAL TRANSDUCTION, 1974 PHOSPHORY LATION, G. POCTEINS, THIOREDOXIN, 3 VISION, MERA, OMBLEX (TRANSDUCER/TRANSDUCTION)	TRANSCRIPTION REGULATION PROTO-ONCOGENE, NUCLEAR BODIES (PODS), LEUKEMIA, 2 TRANSCRIPTION REGULATION
Coumpound	PHOSDUCIN; CHAIN: P;	TRANSDUCIN; CHAIN; P; PHOSDUCIN; CHAIN; P;	TRANSDUCIN; CHAIN: B, C; PHOSDUCIN; CHAIN: P;	TRANSCRIPTION FACTOR PML; CHAIN: NULL;
SEQFOL D score				
PMF		-0.19	-0.20	65.0
Verify		0.29	0.23	-0.68
Psi Blast		1.5e-20	1.5e-13	1.1e-07
END		647	746	55
STAR T AA		513	11.5	29
CHAI N ID		д	e.	
PDB		2trc	2hrc	Ibor
SEQ NO:		1845	1845	1849

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PDB annotation	ACTIN BINDING PROTEIN ABP-120; ACTIN BINDING PROTEIN, STRUCTURE, IMMUNOGLOBULIN, GELATION 2 FACTOR, ABP-120	ACTIN BINDING PROTEIN ABP-120; ACTIN BINDING PROTEIN, STRUCTURE, IMMUNOGLOBULIN, GELATION 2 FACTOR, ABP-120	ACTIN BINDING PROTEIN ABP-120; ACTIN BINDING PROTEIN, STRUCTURE, IMMUNOGLOBULIN, GELATION 2 FACTOR, ABP-120	ACTIN BINDING PROTEIN ACTIN BINDING PROTEIN 120; ACTIN BINDING PROTEIN, BINDING PROTEIN, FACTOR, ABP. 2 120	ACTIN BINDING PROTEIN ACTIN BINDING PROTEIN 120; ACTIN BINDING PROTEIN, IMMUNOGLOBULIN, GELATION FACTOR, ABP. 2 120	ACTIN BINDING PROTEIN ACTIN BINDING PROTEIN 120; ACTIN BINDING PROTEIN, BIMDING PROTEIN, BAMUNOGLOBULIN, GELATION FACTOR, ABP. 2 120	ACTIN BINDING PROTEIN ACTIN BINDING PROTEIN, BINDING PROTEIN, IMMUNOGLOBULIN, GELATION FACTOR, ABP. 2 120	TRANSFERASE
Coumpound	GELATION FACTOR; CHAIN: NULL;	GELATION FACTOR; CHAIN: NULL;	GELATION FACTOR; CHAIN: NULL;	GELATION FACTOR; CHAIN: A, B;	GELATION FACTOR; CHAIN: A, B;	GELATION FACTOR; CHAIN: A, B;	GELATION FACTOR; CHAIN: A, B;	GLYCINE N.
SEQFOL D score	64.85			62.06				
PMF		66.0	1.00		0.95	96.0	66:0	0.21
Verify score		0.47	0.54		0.11	0.52	0.52	-0.00
Psi Blast	4.5e-30	4.5e-30	1.36-19	6e-36	1.66-13	1.3e-19	6e-36	7.5e-06
END	200	498	499	515	494	528	528	331
STAR	397	398	398	306	359	395	397	175
CHAI N ID				<	¥	<	<	A
EDB ID	lksr	1ksr	1ksr	1qfh	lqfh	Iqfh	1qfh	1d2h
SEQ ID NO:	1849	1849	1849	1849	1849	1849	1849	1850

PDB annotation	METHYLTRANSFERASE	STRUCTURAL GENOMICS HYPOTHETICAL PROTEIN, METHANOCOCCUS JANNASCHII	TRANSFERASE SAM-BINDING DOMAIN, BETA-BARREL, MIXED ALPHA-BETA, HEXAMER, 2 DIMER	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT	COMPLEX (TRANSCAPTION REGULATIONDNA) CABRALPHA, CHANSCAPTION TRANSCAPTION TO	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX
Coumpound	METHYLTRANSFERASE; CHAIN: A, B, C, D;	MJ0882; CHAĪN: A;	HNRNP ARGININE N- METHYLTRANSFERASE; CHAIN: 1, 2, 3, 4, 5, 6;	TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	TRANSTREASPHOSPHOTAA NSFRASS PG-AANF DEPENDENT PROTEIN KINASE E.C.2.1.37) GGAMCSI JAPA IGCATALYTE SUBINITIA ALHA SOGREYME MITNAT WITH SOGREYME MITNAT WITH THE PEPTIOL IAMA. THE PEPTIOL IAMA. THE PEPTIOL IAMA. OA BINDIO PROTEIN ABOUTE DETERGENT MEGAA JAPA (E DETERGENT MEGAA JAPA (E DETERGENT MEGAA JAPA (E CHANNE, A; CHANNE) PROTEIN BETA I, CHANNE, DINA; CHANNE D, E	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B;
SEQFOL D score					08/66	
PMF		0.01	0.04	56'0	1.00	1.00
Verify		0.24	0.11	0.39	0.33	0.55
Psi Blast		6.4e-09	1.3e-14	4.5e-32	4.5e-30 1.5e-36	7.5e-43
END AA		294	292	899	349	637
STAR T AA		177	148	538	447	480
CHAI		A	_		ы <u>ш</u>	20
PDB DD		1dus	1g6q	la5e	lapm lawc	lawc
SEQ NO.		1850	1850	1853	1853	1853

PDB annotation	(TRANSCRIPTION REGILATIONDNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRPTON REGILATION/MY, OABPALPHA; GABBETAL; COMPLEX (TRANSCRPTON REGILATION/MA, DNA-BINDING, REGILATION/MA, DNA-BINDING, ANCYTEN REPEAT; TRANSCRPTION 3 FACTOR	COMPLEX (TRANSCRIPTION REGULATIONDYNA OBBALPHA; GABBETAL; COMPLEX (TRANSCRIPTION REGULATIONDNA,) DNA-BINDING, REGULATIONDNA,) DNA-BINDING, ANCYRIN REPELS. TRANSCRIPTION 3 PACTOR.	COMPLEX (TRANSCRIPTION REGILATION/DNA OBBALPHA; OABPETAL; COMPLEX (TRANSCRIPTION) REGILATION/DNA, DNA-BINDING, SNUCLEAR PROTEN, ETS DOMAIN, ANKYRIN REPELS, TRANSCRIPTION 3 PACTOR	COMPLEX (TRANSCRIPTION REGULATIONDNA) GABPALPHA; CABPEETAI; COMPLEX (TRANSCRIPTION REGULATIONDNA), DNA-BINDING,
Coumpound	DNA; CHAIN: D, E;	GA BINDING ROTE IN ALPHA; CHARIN: A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, B;	GA BINDING ROTEIN ALPHA; CARIN: A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E;	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, E;	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;
SEQFOL D score		24.92			
PMF			00'1	1.00	1.00
Verify score			0.72	0.70	0.60
Psi Blast		1.2c-45	6.4e-35	1.2e-45	1.5e-44
END AA		705	704	737	770
STAR T AA		551	556	284	617
CHAI N ID		я	æ	en .	æ
PDB ID		lawc	lawc	lawc	Iawc
SEQ No: D		1853	1853	1853	1853

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PDB annotation	2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA;	GABPBETAI; COMPLEX (TRANSCRIPTION	REGULATION/DNA), DNA-BINDING,	Z NUCLEAK PROTEIN, ETS DOMAIN, ANK YRIN REPEATS,	TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION REGILLATION/DNA) GABPALPHA:	GABPBETA1: COMPLEX	(TRANSCRIPTION	REGULATION/DNA), DNA-BINDING,	2 NUCLEAR PROTEIN, ETS DOMAIN,	ANKYRIN REPEATS,	TRANSCRIPTION 3 FACTOR	COMPLEX (TRANSCRIPTION	REGULATION/DNA) GABPALPHA;	GABPBETAI; COMPLEX	(TRANSCRIPTION	REGULATION/DNA), DNA-BINDING,	2 NUCLEAR PROTEIN, ETS DOMAIN,	ANKYRIN REPEATS,	TRANSCRIPTION 3 FACTOR	COMPLEX (ISOMERASE/PROTEIN	KINASE) FKBP12;	SERINE/THREONINE-PROTEIN	KINASE RECEPTOR R4; COMPLEX	(ISOMERASE/PROTEIN KINASE),	RECEPTOR 2 SERINE/THREONINE	KINASE
Coumpound		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING	PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;				GA BINDING PROTEIN ALPHA; CHAIN: A: GA BINDING	PROTEIN BETA 1: CHAIN: B:	DNA; CHAIN: D, E;					GA BINDING PROTEIN ALPHA;	CHAIN: A; GA BINDING	PROTEIN BETA 1; CHAIN: B;	DNA; CHAIN: D, B;					FK506-BINDING PROTEIN;	CHAIN: A, C, E, G; TGF-B	SUPERFAMILY RECEPTOR	TYPE I; CHAIN: B, D, F, H;			
SEQFOL D score																												
PMF		1.00					1.00							1.00								1.00						
Verify		0.63					0.34							0.74								0.37						
Psi Blast		1.5e-42					1.6e-32							3e-35								3e-49						
END AA		802					802							828								576						
STAR T AA		651					929							687								26						
CHAI		g .					ш							e B								щ						
PDB		lawc					lawc							lawc					_			1b6c						_
SEQ NO:		1853					1853							1853								1853						_

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PDB annotation	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	COMPLEX (INHIBITOR PROTEINKINASS) HIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHABETA, COMPLEX (INHIBITOR PROTEINKINASE)	COMPLEX (INHIBITOR PROTEINKINASE) HHBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHABETA, COMPLEX (INHIBITOR PROTEINKINASE)	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL.					
Coumpound	P19NK4D CDK4/6 INHIBITOR; CHAIN: NULL;	PI9DNK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	PI9DNK4D CDK4/6 INFIBITOR; CHAIN: NULL;	CYCLIN-DEPENDENT KINASE 6, CHAIN: A; PI9INK4D; CHAIN: B;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; PI9INK4D; CHAIN: B;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;
SEQFOL D score									
PMF	0.49	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00
Verify	0.37	99.0	0.58	0.76	0.32	0.51	0.21	0.77	0.63
Psi Blast	4.8e-10	4.5e-35	1.4e-40	1.5e-44	6e-42	1.5e-40	1.1e-36	3e-43	1.5e-41
END	574	902	637	673	739	802	610	673	743
STAR	445	458	486	518	585	652	447	521	587
CHAI N ID							ш	ш	æ
PDB ID	8pq1	1bd8	8pq1	1bd8	8Pq1	1bd8	1blx	1blx	1blx
SEQ NO.	1853	1853	1853	1853	1853	1853	1853	1853	1853

PBB CHAI STAR END Ph Blast Verify Ph StOPO Coumpound							_		_	_		_	_	_			_	_	_	_	_	_	_
PBB CHAI STAR END Phi Blast Verify PMF SEQPOL	PDB annotation	ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT	KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	HORMONE/GROWTH FACTOR P18- INK4C; CELL CYCLE INFIBITOR,	P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR	HORMONE/GROWTH FACTOR P18-	INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR,	CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH PACTOR	TRANSFERASE CSK; PROTEIN	KINASE, C-TERMINAL SRC KINASE, PHOSPHORYLATION, 2	STAUROSPORINE, TRANSFERASE									SIGNALING PROTEIN HELIX-TURN-	HELIX, ANKYRIN REPEAT	SIGNALING PROTEIN HELIX-TURN-
PDB CIAA STAR EVD Pallinat Verify Pallinat Verify Pallinat Secret Secre	Coumpound		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P191NK4D; CHAIN: B;		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;		CYCLIN-DEPENDENT KINASE	6 INHIBITOR; CHAIN: A;		C-TERMINAL SRC KINASE;	CHAIN: A;		PHOSPHOTRANSFERASE	CAMP-DEPENDENT PROTEIN	KINASE CATALYTIC SUBUNIT	TRANSFERASE/PHOSPHOTRA	NSFERASE) CAMP-	DEPENDENT PROTEIN KINASE	(E.C.2.7.1.37) (CAPK) 1CTP 3	(CATALYTIC SUBUNIT) 1CTP 4	CYCLIN-DEPENDENT KINASE	4 INHIBITOR B; CHAIN: A;	CYCLIN-DEPENDENT KINASE
PB CHAI STAR END Fal Blast Verify	SEQFOL D score						İ						96.05			92.53							
Prop. CHAI STAR END Pal Blast ID N ND TAA AA Pal Blast Ibix B 651 808 4.5c-41 C Ibix B A 444 576 8c-69 C Ibix B A 24 276 1.4c-45 C Icix B B A 24 276 1.5c-30 C C 25c-33 C C 25c-33 C C 25c-33 C 25c	PMF		0.1		0.87		1.00			86:0											1.00		1.00
PBB CIGAI STAR END N D N D TAA AA	Verify score		09.0		0.16		09.0			0.81											0.73		0.36
PB CHAI STAR ID NID TAA Ibis A 444 Ibis A 444 Ibis A 446 Ibis			4.5e-41		60-28		4.5e-33			1.4e-45			1.5e-30			1.5e-30					le-35		1.5e-33
Pre CHAI	END		808		976		612			276			349			342					019		637
1 D 1 D 1 D 1 D 1 D 1 D 1 D 1 D 1 D 1 D	STAR		651		444		486			24			_			-					478		510
	CHAI		e e		∢		A			¥			ш			Ξ					٧		A
SBRQ NO. NO. NO. NO. NO. NO. NO. NO. NO. NO.	PDB TD		Iblx		1bu9		1bu9			1byg			lcmk			Ictp					1498		1d9s
	SEQ No.		1853		1853		1853			1853			1853			1853					1853		1853

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PDB annotation	HELIX, ANKYRIN REPEAT	SIGNALING PROTEIN HELIX-TURN- HELIX ANKYRIN REPEAT	SIGNALING PROTEIN HELIX-TURN-	FELLA, ANA TRIN REPEAT	SIGNALING PROTEIN FIELLX-1 URN- HELIX, ANKYRIN REPEAT	SIGNALING PROTEIN HELIX-TURN- HELIX, ANKYRIN REPEAT	METAL BINDING PROTEIN ZINC-	BINDING MODULE, ANKYRIN	REPEATS, METAL BINDING	PHOSPHOTE A NSFER A SF FGER IK	FIREORI AST GROWTH EACTOR	RECEPTOR 1: TRANSFERASE	TYROSINE-PROTEIN KINASE ATP-	BINDING, 2 PHOSPHORYLATION.	RECEPTOR.	PHOSPHOTRANSFERASE	PHOSPHOTRANSFERASE FGFRIK,	FIBROBLAST GROWTH FACTOR	RECEPTOR I; TRANSFERASE,	TYROSINE-PROTEIN KINASE, ATP-	BINDING, 2 PHOSPHORYLATION,	RECEPTOR,	PHOSPHOTRANSFERASE	PHOSPHOTRANSFERASE FGFRIK,	FIBROBLAST GROWTH FACTOR	RECEPTOR 1; TRANSFERASE,	TYROSINE-PROTEIN KINASE, ATP-	BINDING, 2 PHOSPHORYLATION,	RECEPTOR, PHOSPHOTRANSFERASE
Compound	4 INHIBITOR B; CHAIN: A;	CYCLIN-DEPENDENT KINASE 4 INHIBITOR B: CHAIN: A:	CYCLIN-DEPENDENT KINASE	OVOT INTERPREDICT VINTAGE	4 INHIBITOR B; CHAIN: A;	CYCLIN-DEPENDENT KINASE 4 INHIBITOR B: CHAIN: A:	PYK2-ASSOCIATED PROTEIN	BETA; CHAIN: A;		EGF RECEPTOR 1. CHAIN: A B:	to the state of the state of the						FGF RECEPTOR I; CHAIN: A, B;							FGF RECEPTOR 1; CHAIN: A, B;					
SEQFOL D score										114.87	10.1.1													112.87					
PMF score		I.00	1.00	100	1:00	0.92	0.51										00:I												
Verify		0.65	0.36	0.40	C+.0	0.54	0.13										0.46												
Psi Blast		7.5e-38	9e-37	10-04	1.25-34	3e-34	4.5e-32			1.50-45	}						1.5e-45							7.5e-45					
END		673	743	255	?	807	694			203	3						276							292					
STAR T AA		545	809	24.5	£	677	513			8	:						26				_			_					
CHAI N ID		Ą	4		<	4	Ą			A	:						A							В					
FDB		s6p1	s6pt	Tabo	SGDI	S6P1	Idea			1fok	5						1fgk							Ifgk					
SEQ NO:		1853	1853	1050	26	1853	1853			1853	}						1853							1853					

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PDB annotation	PHOSPHOTRANSEERASE FGFRIK, FIBROBLAST GROWTH FACTOR RECEPTOR I; TRANSFERASE, TYROSINE-PROTEIN KINASE, AIP- BINDING, 2 PHOSPHOR VLATION, RECEPTOR,	PHOSPHOTRANSFERASE C-SRC, PG-SRC, SRC, TYGOSINE KINASE, PHOSPHOR YLATION, SR2, SR3, 2 PHOSPHOTYROSINE, PROTO- ONCOGENE, PHOSPHOTRANSFERASE	TRANSFERASE P150, C-ABL; KINASE, KINASE INHIBITOR, STI- 571, ACTIVATION LOOP	PROTEIN KINASE CDK2; TRANSFERASE, SERNIE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION	CELL CYCLE INHIBITOR P18- INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), MAYYRIN REPEAT, 2 CDK 4/6 INHIBITOR.	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKBAFKB COMPLEX	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
Coumpound	FGF RECEPTOR I; CHAIN: A, B;	TYROSINE-PROTEIN KINASE SRC; CHAIN: NULL;	PROTO-ONCOGENE TYROSINE-PROTEIN KINASE ABL; CHAIN: A, B;	HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA- B-ALPHA; CHAIN: D;	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-
SEQFOL D score				92.94			
PMF	1:00	1:00	1.00		1:00	00'1	1:00
Verify score	0.50	0.79	0.51		0.36	0.41	0.41
Psi Blast	7.5e-45	1.2e-46	7.5e-45	9e-28	3e-34	4.5e-46	6e-53
END	276	276	276	326	809	647	089
STAR	26	56	49	61	484	458	486
CHAI N ID	м		V		∢	D	Ω
EDB ID	lfgk	Ifink	Ifpu	Ihcl	lihb	likn	likn
SEQ No.	1853	1853	1853	1853	1853	1853	1853

	2000	2			
				B-ALPHA; CHAIN: D;	
66-58	0.21	1.00		NF-KAPPA-B P65 SUBUNIT;	TRANSCRIPTION FACTOR P65;
				CHAIN: A; NF-KAPPA-B P50D	P50D; TRANSCRIPTION FACTOR,
				SUBUNIT; CHAIN: C; I-KAPPA- B-ALPHA; CHAIN: D;	IKB/NFKB COMPLEX
4.5e-52	0.26	1.00		NF-KAPPA-B P65 SUBUNIT;	TRANSCRIPTION FACTOR P65;
				CHAIN: A; NF-KAPPA-B P50D	P50D; TRANSCRIPTION FACTOR.
				SUBUNIT; CHAIN: C; I-KAPPA- B-AI,PHA: CHAIN: D:	IKB/NFKB COMPLEX
1.3e-54	0.15	00.1		NF-KAPPA-B P65 SUBUNIT;	TRANSCRIPTION FACTOR P65;
_				CHAIN: A; NF-KAPPA-B P50D	P50D; TRANSCRIPTION FACTOR,
				SUBUNIT; CHAIN: C; I-KAPPA- B-ALPHA; CHAIN: D;	IKB/NFKB COMPLEX
1.5e-46			114.32	INSULIN RECEPTOR; CHAIN: A;	COMPLEX
_				PEPTIDE SUBSTRATE; CHAIN:	
				Ď.	TYROSINE KINASE, SIGNAL
					TRANSDUCTION,
					PHOSPHOTRANSFERASE, 2
					COMPLEX (KINASE/PEPTIDE
					SUBSTRATE/ATP ANALOG),
					ENZYME, 3 COMPLEX
1		1			-
1.56-40	0.65	3.		INSULIN RECEPTOR; CHAIN: A;	÷
				PEPTIDE SUBSTRATE; CHAIN:	(TRANSFERASE/SUBSTRATE)
				B:	TYROSINE KINASE, SIGNAL
					TRANSDUCTION,
					PHOSPHOTRANSFERASE, 2
					COMPLEX (KINASE/PEPTIDE
					SUBSTRATE/ATP ANALOG),
					ENZYME, 3 COMPLEX
					(TRANSFERASE/SUBSTRATE)
8e-13	0.46	0.93		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN,
9e-23	0.46	8		MYOTROPHIN: CHAIN: NITI 1	ANK PEPEAT MYOTOODHIN
	1.3e-46 1.3e-46 1.3e-46 1.9e-23	1.3e-46 .0.65 1.3c-46 .0.65 8e-13 0.46	9 9	0.065 1.00 0.46 0.035 0.46 0.035	6 0.65 1.00 0.46 0.93 0.46 1.00

PDB annotation	ACETYLATION, NMR, ANK-REPEAT	ANK-REPEAT MYOTROPHIN, ACETYLATION, NAR, ANK-REPEAT	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR. ANK-REPEAT	COMPLEX (TRANSCRIPTION	(TRANSCRIPTION	REGULATION/ANK REPEAT),	ANK YKIN Z KEPEAT HELLX	COMPLEX (TRANSCRIPTION	CTRANSCRIPTION	REGULATION/ANK REPEAT),	ANKYRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION	REG/ANK REPEAT) COMPLEX	(TRANSCRIPTION	REGULATION/ANK REPEAT),	ANKYRIN 2 REPEAT HELIX	COMPLEX (TRANSCRIPTION	REGANK REPEAT) COMPLEX	(TRANSCRIPTION	REGULATION/ANK REPEAT),	COMPLEX (TRANSCRIPTION
Coumpound		MYOTROPHIN; CHAIN: NULL	MYOTROPFIIN; CHAIN: NULL	MYOTROPHIN; CHAIN: NULL	MYOTROPHIN; CHAIN: NULL	MYOTROPHIN; CHAIN: NULL	MYOTROPHIN; CHAIN: NULL	NF-KAPPA-B P65; CHAIN: A, C;	I-KAPPA-B-ALPHA; CHAIN: E,	př.		NF KAPPA-B P65; CHAIN: A, C;	I-KAPPA-B-ALPHA: CHAIN: B, D;	Œ,		NF-KAPPA-B P65; CHAIN: A, C;	NF-KAPPA-B P50; CHAIN: B, D;	I-KAPPA-B-ALPHA; CHAIN: E,	ė.		NF-KAPPA-B P65; CHAIN: A, C,	NF-KAPPA-B P30; CHAIN: B, D;	I-KAPPA-B-ALPHA; CHAIN: E,	:£4	NF-KAPPA-B P65; CHAIN: A, C;
SEQFOL D score			-													_									
PMF		0.46	1.00	1.00	66.0	0.57	1.00	1.00				00.1				00.1					96.				1.00
Verify		-0.06	0.55	0.44	0.34	-0.03	0.37	0.50			0	0.52				0.54					0.20				0.56
Psi Blast		8e-16	4.5e-32	1.5e-36	1.5e-32	3e-33	1.5e-30	6e-43				3e-20				1.2e-53					1.56-53				1.5e-53
END		589	635	699	735	768	008	637			Contra	//0				749				0.00	8/				815
STAR T AA		461	521	554	621	654	684	461			1	484				549				, 0	281				919
CHAI N ID								ш			,	n				ш					מ				ы
PDB UD		lmyo	1myo	1туо	lmyo	1myo	lmyo	Jul				H				Ħ			_	0.1	=	_			lnfi
SEQ NO:		1853	1853	1853	1853	1853	1853	1853			000	1833				1853				0.00	1833				1853

PDB annotation	REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE; TRANSFERASE, MAP KINASE, SERINE/TEREONINE-PROTEIN KINASE, 278	TRANSFERASE MAP KINASE, SERINE/THREONINE PROTEIN KINASE, TRANSPERASE	TYROSINE KINASE TYROSINE KINASE-INHIBITOR COMPLEX, DOWN-REGULATED KINASE, 2 ORDERED ACTIVATION LOOP	TRANSFERASE ALPHA BETA FOLD TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ANKYRIN REPEATS, CELL-CYCLE	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ANKYRIN REPEATS, CELL-CYCLE	ONCOCRETE (AURT) PSSR2, ANK YRIN REPEATS) PSSR2, ANK YRIN REPEATS, PSSR2, ANK YRIN REPEATS, AUGUST SUPPRESSOR, AUGUST PROPER PROPERTY, DISCREDIT, PROCEDURATY, NUCLEAR DISCREDIT, PROCEDURATY, ONCOCREDIT, ONCOCRE	COMPLEX (ANTI- ONCOGENE/ANKYRIN REPEATS)
Coumpound	NF-KAPPA-B P50, CHAIN; B, D; RE I-KAPPA-B-ALPHA; CHAIN; E, RE F; AND PF	MAP KINASE P38; CHAIN: TR NULL; AC TR SEE SEE KINASE P38; CHAIN: TR KIN	ERK2; CHAIN: NULL; TR SEI KII	HAEMATOPOETIC CELL TY KINASE (HCK); CHAIN: A; KI) DO OR	LCK KINASE, CHAIN: A; TR REGULATORY PROTEIN SWI6; TR CHAIN: A, B; TR	REGULATORY PROTEIN SWI6; TR CHAIN: A, B; TR	P55, CHAIN: A, 53BP2, CHAIN: OO B; P55, CHAIN: A, 53BP2, CHAIN: DO	P53; CHAIN: A; 53BP2; CHAIN: CO B;
SEQFOL D score		92.67	97.49					
PMF				1.00	0.10	0.00	96:0	1.00
Verify				0.66	-0.40	-0.17	0.27	0.31
Psi Blast		3e-27	6e-29	1.5e-49	7.5e-50 1.5e-17	1.5e-40	3.26-12	6.4e-12
END		359	358	276	592	759	503	578
STAR T AA		4	15	56	26 466	512	452	458
CHAI N ID				¥	A A	<	m	В
EDB ID		1p38	Ipme	Iqef	lqpc 1sw6	1sw6	1ycs	1yes
SEQ NO:		1853	1853	1853	1853	1853	1853	1853

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PDB annotation	PS3BP2, ANKYRUN REPEĂTS, SH3, PS3, TUMOR SUPPRESSOR, MALLITGENE Z FAMILY, NICLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-	ONCOGENEZA (ANTERNETATION) ONCOGENEZA (ANTERNETATION) PESTAPEZ, ANTERNETATION, SHI, PESTAPEZ, ANTERNETATION, STORITH, PHOSPEROTATION, DISTABLE SE MAITTATION, DISTABLE MAITTATION, ONCOGENEZA (ANTERNETATION) ONCOGENEZA (ANTERNETATION)	ONCOGENEZA (ANT) ONCOGENEZA (ANT) STESTOP, ANT/STRIN REPEATS, SHI, FRSTIPE, ANT/STRIN REPEATS, SHI, FRSTIPE, ANT/STRIN REPEATS, SHI, FRSTIPE, ANT/STRIN REPEATS, SHI, FRSTIPE, ANT/STRIN REPEATS ONCOGENEZA (ANT) ONCOGENEZA (ANT) ONCOGENEZA (ANT) ONCOGENEZA (ANT) ONCOGENEZA (ANT)	ONCOGENERA (ANT) ONCOGENERA (ANT) SESSPE, ANK TRIN REPEATS, SH3, PE3, TUMOR SUPPLESSOR, MULTIGENE PEATS, SH4, PE3, TUMOR SUPPLESSOR, MULTIGENE PEAMITY, MUCLEAR PORTING, HORSENG PRANTATION, DISEASE MUTATION, 3 ONCOGENERAL COMPLEX (ANT) ONCOGENERAL (STREATS)
Coumpound		P53, CHAIN: A; 53BP2; CHAIN: B;	P33, CHAIN: A; 53BP2; CHAIN: B;	P33, CHAIN: A; 53BP2; CHAIN: B;
SEQFOL D score				
PMF		0.99	66'0	0.30
Verify score		0.09	0.26	-0.13
Psi Blast		6e-33	1.46-38	7.56-33
END		099	726	608
STAR T AA		88	554	654
CHAI N ID		ш	Д	д
PDB ID		lyes	lycs	lycs
SEQ No.		1853	1853	1853

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PDB annotation	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE, MAP 2, ERK2; TRANSFERASE, SERNBETHREONING-PROTEIN KINASE, MAP KINASE, 2 ERK2	SIGNALING PROTEIN GTP-BINDING PROTEINS, PROTEIN-PROTEIN COMPLEX, EFFECTORS	SIGNALING PROTEIN GTP-BINDING PROTEINS, PROTEIN-PROTEIN COMPLEX, EFFECTORS	SIGNALING PROTEIN G PROTEIN, GTP HYDROLYSIS, KINETIC CRYSTALLOGRAPHY, 2 SIGNALING PROTEIN	SIGNALING PROTEIN G PROTEIN, GTP HYDROLYSIS, KINETIC CRYSTALLOGRAPHY, 2 SIGNALING PROTEIN	ENDOCYTOSIS/EXOCYTOSIS G- PROTEIN, GTPASE, RAB6, VESICULAR TRAFFICKING	SIGNALINO PROTERD P21-RAC2; RHO GDT2, RHO-GDI BETA, LY-GDI; BETA SANDWHICH, PROTEIN- PROTER COMPLEX, C-DOMAIN, 2 IMMUNOGLOBULIN FOLD, WALKER FOLD, GTP-BINDING
Coumpound	EXTRACELLULAR REGULATED KINASE 2; CHAIN: NULL;	RAS-RELATED PROTEIN RAP- 1A; CHAIN: A; PROTO- ONKOGENE SERNACHIREONINE PROTEIN KINASE CHAIN: B:	RAS-RELATED PROTEIN RAP- 1A; CHAIN: A; PROTO- ONROGENE SERINETTHEONINE PROTEIN KINASE CHAIN: B;	TRANSFORMING PROTEIN P21/H-RAS-1; CHAIN: A;	TRANSFORMING PROTEIN P21/H-RAS-1; CHAIN: A;	RAB6 GTPASE; CHAIN: A;	RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 2; CHAIN: A; RHO GDP-DISSOCIATION INHIBITOR 2; CHAIN: B;
SEQFOL D score	107.86	85.26			77.02		
PMF score			1.00	1.00		1.00	0.59
Verify			0.43	0.55		0.48	0.12
Psi Blast	9e-31	9.6e-68	9.66-68	1.6e-68	1.6e-68	6.4e-56	3.2e-53
END	356	171	173	173	174	171	176
STAR T AA	'n	_	_	_	_	6	-
CHAI N ID		4	<	<	∢	٧	¥
EDB EDB	3erk	lely	lely	lctq	letq	1450	9sp1
SEQ NO.	1853	1854	1854		1854		1854

	F			_		1		
PDB annotation	ENDOCYTOSIS/EXOCYTOSIS G PROTEIN, VESICULAR TRAFFIC, OTP HYDROLYSIS, YPT/RAB 2 PROTEIN, ENDOCYTOSIS, HYDROLASE	GTP-BINDING PROTEIN GTP. BINDING PROTEIN, SMALL G PROTEIN, RAP2, GDP, RAS	GTP-BINDING PROTEIN GTP- BINDING PROTEIN, SMALL G PROTEIN, RAP2, GDP, RAS	GTP-BINDING GTP-BINDING, GTPASE, SMALL G-PROTEIN, RHO FAMILY, RAS SUPER 2 FAMILY	GTP-BINDING GTP-BINDING, GTPASE, SMALL G-PROTEIN, RHO FAMILY, RAS SUPER 2 FAMILY		COMPLEX (SMALL GTPASENUCLEAR PROTEIN) COMPLEX (SMALL GTPASENUCLEAR PROTEIN), SMALL GTPASE, 2 NUCLEAR TRANSPORT	COMPLEX (GTP- BINDING/EFFECTOR) RAS-RELATED PROTEIN RAB3A; COMPLEX (GTP-
Coumpound	GTP-BINDING PROTEIN YPT51; CHAIN: A;	RAP2A; CHAIN: NULL;	RAP2A; CHAIN: NULL;	RACI; CHAIN: NULL;	RACI; CHAIN: NULL;	ONCOGENE PROTEIN CHARAS P21 PROTEIN MUTANT WITH GLY 12 REPLACED BY PRO H13 (GLEY) COMPLEXED WITH P2-1-Q. NITROPHENYLJETHYL. IPLJ 4 GRANGSING-SCH, GRANDO)- TRIPHOSPHATE IPLJ 5 TRIPHOSPHATE IPLJ 5	RAN; CHAIN: A, C; NUCLEAR PORE COMPLEX PROTEIN NUP358; CHAIN: B, D;	RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;
SEQFOL D score			95.27	52.65			50.36	60.15
PMF	0.1	00.1			0.94	0.01		
Verify score	0.31	0.49			0.28	0.37		
Psi Blast	6.4e-55	4.8e-64	4.8e-64	1.1e-53	1.1e-53	4.8e-52	4.8e-36	8c-59
END	174	171	174	174	9/1	171	186	179
STAR T AA	1	-	1	_	2	-	2	1
CHA1 N ID	٧						၁	٧
FDB TD	1ek0	lkao	1kao	1mh1	lmfl l	ilqi	dir.	1zbd
SEQ No:	1854	1854	1854	1854	1854	1854	1854	1854

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PDB annotation	BINDING/BEFECTOR), G PROTEIN, EFFECTOR, RABCDR, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN, RAB3A, RABPHILIN	COMPLEX (GTP- BINDINGEFFECTOR) RAS-RELATED PROTEIN RABA; COMPLEX (GTP- BINDINGEFFECTOR), G PROTEIN, EFFECTOR, RABCING, 2 SYNAPTIC EXOCYTOSIS, RAB PROTEIN,	HYDROLASE CDC42/CDC42GAP; CDC42/CDC42GAP; TRANSITION STATE, G-PROTEIN, GAP, CDC42, ALF3., HYDROLASE	HYDROLASE G PROTEIN, VESICULAR TRAFFICKING, GTP HYDROLYSIS, RAB 2 PROTEIN, NEUROTRANSMITTER RELEASE, HYDROLASE	HYDROLASE GPROTEIN, SESICULAR TRAFFICKING, GTP HYDROLYSIS, RAB 2 PROTEIN, NEUROTRANSMITTER RELEASE, HYDROLASE	COMPLEX (SERINE PROTEASE/INHEIDTOR) SKIN- BROTEASE/INHEIDTOR) SKIN- BROTEASE, INTORIANSE, SERINE PROTEASE, INTORIANSE, SERINE COMPLEX (SERINE PROTEASE, INTORIANSE, COMPLEX (SERINE
Commpound		RAB-3A; CHAIN: A; RABPHILIN:3A; CHAIN: B;	GTP BINDING PROTEIN (G25K); CHAIN: A: GTPASE ACTIVATING PROTEIN (RHG); CHAIN: B:	RAB3A; CHAIN: A;	RAB3A; CHAIN: A;	CHAIN: E, ELATIN; COMPLEX (SERING CHAIN: E, ELATIN; COMPLEX CHAIN: E, ELATIN; PROTEASE, PEROTEASE, PEROTEASE, DASTR ZYMOCHE TAX ZYMOCHE TAX (SERING PROTEASE), PAROTEASE, PAROTE
SEQFOL D score			54.33	68.59		
PMF		0.96			0.99	0.48
Verify		0.43			0.27	-0.71
Psi Blast		86-59	3.2e-50	1.16-59	1.1e-59	3.2e-16
END		9/1	193	174	174	27
STAR		4	-	2	4	33
CHAI N ID		⋖	V	V.	V	_
rog m		1zbd	2ngr	3rab	3rab	1fle
SEQ No no		1854	1854	1854	1854	1856

PDB annotation	BINDING, MEMBRANE TRAFFICKIN, NON-MYRISTOYLATED 1HUR 16	GTP-BINDING PROTEIN GTP- BINDING PROTEIN, SMALL G PROTEIN, RAP2, GDP, RAS	COMPLEX(GTPASE ACTIVATIVROTO-ONCOGENE) GTPASE-ACTIVATING PROTEIN RHOGAP; COMPLEX (GTPASE ACTIVATION PROTO-ONCOGENE) GTPASE 2 TRANSITION STATE. GAP	HYDROLASE G PROTEIN, VESICULAR TRAFFICKING, GTP VESICULAR TRAFFICKING, GTP VEDROLYSIS, RAB 2 PROTEIN, NEUROTRANSMITTER RELEASE, HYDROLASE		COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN PROTEIN	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CR YSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
Соитроинд	FACTOR 1; 1HUR 5 CHAIN: A, B; 1HUR 7	RAP2A; CHAIN: NULL;	P50-RHOGAP, CHAIN: A; TRANSFORMING PROTEIN RHOA; CHAIN: B;	RAB3A; CHAIN: A;		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE: CHAIN: B. C:	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE: CHAIN: B, C:	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;
SEQFOL D score		50.54					58.29		
PMF			-0.03	0.30		0.28		0.51	60.0
Verify			0.22	-0.03		-0.07		0.40	-0.22
Psi Blast		1.6e-24	1.6e-27	3.2e-33		3.2e-30	3.2e-31	3.2e-31	3.2e-50
END		981	581	190		132	162	091	188
STAR T AA		61	ខ	22		22	92	8	107
CHAI N ID			ш	×		∢	٧	∀	υ
FDB TD		1kao	ltx4	3rab	_	la l	lalh	lath	Imey
SEQ No D		1857	1857	1857		1858	1858	1858	1858

PDB annotation	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX CZNC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 RYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (TRANSCRPTTON REGULATION/DNA) TFIIIA; SS GENE, NINR, TFIIIA, PROTEIA, DNA, TRANSCRPTTON FACTOR, SS RAA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRPTION)	COMPLEX (TRANSCRIPTION REGULATION/DIM) YING-YANG I; TRANSCRIPTION INITIATION, INITIATION, INITIATION, ENGREE PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION RECOGNITION, 3 COMPLEX (TRANSCRIPTION)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-
Coumpound	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN; A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	TRANSCRPTION PACTOR IIIA; CHAIN: A, SS RNA GENE; CHAIN: E, F;	VYI; CRAIN; C, ADBNO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DIM; CHAIN; A, B;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;
SEQFOL D score			62.32			
PMF	0.17	86'0		0.24	0.39	0.10
Verify	-0.18	0.17		0.14	-0.08	-0.10
Psi Blast	4.8e-50	1.4e-50	1.4e-50	3.2e-20	1.3e-34	3.2e-33
END	132	160	161	160	160	162
STAR	21	62	82	08	99	=
CHAI N ID	o	ပ	o	A	o	Ą
PDB 1D	lmey	Imey	Imey	143	lubd	2gli
SEQ NO ID	1858	1858	1858	1858	1858	1858

PDB annotation	BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI;	GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-	BINDING PROTEIN/DNA)	COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA),	ZINC FINGER, DNA-BINDING	PROTEIN	COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA),	ZINC FINGER, DNA-BINDING	COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA)	ZINC FINGER DNA-RINDING	PROTEIN	COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA),	ZINC FINGER, DNA-BINDING	PROTEIN	COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA),	ZINC FINGER, DNA-BINDING	PROTEIN	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX
Coumpound	A Community	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;		ZINC FINGER PROTEIN GLII;	CHAIN: A; DNA; CHAIN: C, D;		QGSR ZINC FINGER PEPTIDE;	CHAIN: A; DUPLEX	OLIGONUCLEOTIDE BINDING	SITE; CHAIN: B, C;	OGSR ZINC FINGER PEPTIDE;	CHAIN; A; DUPLEA	OLIGONOCLEOTIDE BINDING	OGSR ZINC FINGER PEPTIDE	CHAIN: A: DIPLEX	OLIGONITCLEOTIDE BINDING	SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE;	CHAIN: A; DUPLEX	OLIGONUCLEOTIDE BINDING	SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE;	CHAIN: A; DUPLEX	OLIGONUCLEOTIDE BINDING	SITE; CHAIN: B, C;	DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PRUIEIN; CHAIN; C, F, G;
SEQFOL D score		58.21					01.09																					
PMF				0.11							0.78			0.35	}			-0.13				0.10				00.1		
Verify score				-0.37							-0.04			-0.23	1			0.07				-0.26				-0.03		
Psi Blast		4.8e-34		4.8e-34			6.4e-29				6.4e-29			4.8e-27	i			6.4e-15				3.2e-25				1.6e-50		
END		188		188			198				197			237	i			273				169				197		
STAR T AA		51		59			115				117			145				212				%				911		
CHAI N ID		V		٧			¥				∢			A				٧				A				υ υ		
PDB ID		2gli		2gli			lalh			1	lalh			lalh				lalh				lalh				Imey		
SEQ ID NO:		1858		1858			1859			7	1859			1859		_		1859				1859				1829		

PDB annotation	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	COMPLEY (ZINC PRICED (DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGENDINA)		
Coumpound		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	PROTEN; CHAIN: C, F, G;		DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;		DNA: CHAM: A B D E.	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			DNA; CHAIN: A. B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;		!	DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;		TO A NICOB INCIDENCE AT A STOCK AT	VEAST TRANSCRIPTION	FACTOR ADRI (RESIDUES 130 -
SEQFOL D score		70.79																												
PMF					0.43				0.10	1				0.00					0.35					0.42				100	0.0	
Verify					-0.02				-0.35					-0.22					-0.10					-0.11				0.00	1	
Psi Blast		1.6e-50			I.3e-46				1 10-33	25.11				1.4e-26					1.1e-41					1.4e-11				90.00	2	
END		861			237				365	}				141					169					237				330	ì	
STAR T AA		911			144				173	!				85					88					509				212	2	
CHAI		ာ			၁				ر)				၁					<u>۔</u>					0						
PDB ID		Imey			lmey				Imen	ì				Imey			_		Imey					Imey	_			Page	Ļ	
SEQ NO:		6581			1859				1850					1859					1829					1859				1850	ì	

PDB annotation		ZINC FINGER TRANSCRIPTION FACTOR SPI; ZINC FINGER, TRANSCRIPTION ACTIVATION, SPI	COMPUTATION CONFIDENCE TO COMPUTATION REGULATION/DNA) TRIIIA; SE ROBER; DNA, TRANSCRIPTON FROTEN, DNA, TRANSCRIPTON FROTEN, SRAN 2 GENE, DNA BRODNO PROTEIN, CINGEN, COMPLEX 3 (TRANSCRIPTON REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) TFIII4; SI GENE; MAR, TFIII4, ROTEIN, DNA, TRANSCRIPTION FROTEIN, DNA, GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION FREGULATION/DNA)	COMPLEX (TRANSCREPTION REGULATION/DONA) TEILIA; SS GENE; NMR, TEILIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, SS RNA 2 GENE, DNA BINDING PROTEIN, ZING FINGER, COMPLEX 3 TRANSCREPTION
Coumpound	189) IPAA 3 (PAZA - CARBOXY TERMINAL ZINC IPNGER DOMAIN) MUTANT WITH IPAA HO 131 REPLACED BY ALA, HO 133 A SEPLACED BY CYS 140 IPAA 5 REPLACED BY CYS 140 IPAA 5 REPLACED BY (NMR, 10 STRUCTURES) IPAA 6	SP1F2; CHAIN: NULL;	TRANSCRIPTON FACTOR IIIA. CHAIN: A; S RNA GENE; CHAIN: E, F.	TRANSCRPTON FACTOR IIIA; CHAIN: A, SS RNA GENE; CHAIN: E, F;	TRANSCRIPTION FACTOR IIIA; CHAIN: A; SS RNA GENE; CHAIN: E, F;
SEQFOL D score				55.20	
PMF		0.03	0.00		0.48
Verify		-0.25	-0.52		-0.08
Psi Blast		3.2e-05	1.1e-I6	1.4e-20	1.4c-20
END		239	169	201	198
STAR T AA		212	105	114	117
CHAI N ID			∢	4	¥
EDB DE		1sp2	91	£#1	103
SEQ No.		6581	1859	1859	1859

PDB annotation	REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX	(TRANSCRIPTION	REGULATION/DNA), RNA	POLYMERASE III, 2	TRANSCRIPTION INITIATION, ZINC	FINGER PROTEIN	COMPLEX (TRANSCRIPTION REGIT ATTOMONA) COMPLEY	(TRANSCRIPTION	REGULATION/DNA), RNA	POLYMERASE III, 2	TRANSCRIPTION INITIATION, ZINC	FINGER PROTEIN	COMPLEX (TRANSCRIPTION	REGULATION/DNA) COMPLEX	(IKANSCRIPTION	REGULATION/DNA), RNA	POLYMERASE III, 2	TRANSCRIPTION INITIATION, ZINC	FINGER PROTEIN	COMPLEX (TRANSCRIPTION	REGULATION/DNA) COMPLEX	(TRANSCRIPTION	REGULATION/DNA), RNA	POLYMERASE III, 2	TRANSCRIPTION INITIATION, ZINC	COMPLEY (The ANICODIMATION)	REGIL ATTON/DNA) YING-YANG 1-	TRANSCRIPTION INITIATION,	INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN
Coumpound		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE;	CHAIN: B, C, E, F;					TEIIIA; CEAIN: A, D; 58 RIBOSOMAT RNA GENE-	CHAIN: B. C. E. F.					TFIIIA; CHAIN: A, D; 5S	RIBOSOMAL RNA GENE;	CHAIN: B, C, E, F;					TFIIIA; CHAIN: A, D; 5S	RIBOSOMAL RNA GENE;	CHAIN: B, C, E, F;				VVI: CHAIM C. ADENO	ASSOCIATED VIRIIS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;
SEQFOL D score														98.99																
PMF		0.10						0.33													0.01						27.0	2		
Verify		-0.24						-0.01													-0.25						000	3		
Psi Blast		1.4e-28						1.1c-28						1.1e-28							3.2e-16						30.22	1		
END		239						275						237							178						220	ì		
STAR T AA		105						117						20							98						110			
CHAI N ID		V						∢						<							∀						L	_		
PDB		1466						911						1116							1119						pqui			
SEQ NO: D		1859						1859						1859							1859.						1850			

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PDB annotation	RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1;	TRANSCRIPTION INITIATION, BUTTATOR ELEMENT XVI ZINC 2	FINGER PROTEIN, DNA-PROTEIN	RECOGNITION, 3 COMPLEX	(TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-YANG 1;	TRANSCRIPTION INITIATION,	INITIATOR ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-PROTEIN	RECOGNITION, 3 COMPLEX	(TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) YING-YANG 1;	TRANSCRIPTION INITIATION,	INITIATOR ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-PROTEIN	RECOGNITION, 3 COMPLEX	(TRANSCRIPTION	REGULATION/DNA)	TRANSCRIPTION REGULATION	TRANSCRIPTION REGULATION,	ADR1, ZINC FINGER, NMR	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-FINGER GLI;	GLI, ZINC FINGER, COMPLEX (DNA-	B NDING BBOTEIN/DNA)
Coumpound		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CIDAIN, A, D,			YYI; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;					YY I; CHAIN: C; ADENO-	ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;					ADRI; CHAIN: NULL;			ZINC FINGER PROTEIN GLII;	CHAIN: A; DNA; CHAIN: C, D;		
SEQFOL D score							68.47																						
PMF		0.07													86.0								0.37			0.33			
Verify		-0.06													-0.27								-0.05			-0.22			
END Psi Blast AA		3.2e-22					3.2e-33							1	3.2e-33								3.2e-16			6.4e-33			-
		265					861								197								171			661			_
STAR T AA		152					98								23								117			106			_
CHAI N ID		υ					o								ر د											¥			
PDB ID		Iubd					Inbd								Inbd								2adr			2gli			
SEQ B Si Si Si Si Si Si Si Si Si Si Si Si Si S		1859					1859								1859								1859			1829			

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PDB annotation	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)		COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA),	ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DIAJ), ZINC FINGER, DNA-BINDING	PROTEIN	COMPLEX (ZINC FINGER/DNA)	ZINC FINGER, DNA-BINDING PROTEIN	GENE REGULATION POZ DOMAIN;	PROTEIN-PROTEIN INTERACTION	DOMAIN, TRANSCRIPTIONAL 2	REPRESSOR, ZINC-FINGER PPOTEIN X-PAV	CRYSTALLOGRAPHY, 3 PROTEIN	STRUCTURE, PROMYELOCYTIC	LEUKEMIA, GENE REGULATION	GENE REGULATION POZ DOMAIN;	DOMAIN, TRANSCRIPTIONAL, 2	REPRESSOR, ZINC-FINGER PROTEIN X-RAY
Coumpound	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;		QGSK ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX	OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE;	OLIGONUCLEOTIDE BINDING	SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A: DUPLEX	OLIGONUCLEOTIDE BINDING SITE: CHAIN: B. C.	PROMYELOCYTIC LEUKEMIA	ZINC FINGER PROTEIN PLZF;	CHAIN: A;					PROMYELOCYTIC LEUKEMIA	CHAIN: A:	
SEQFOL D score	68.84					10'69												64.40		
PMF		0.04		20.1					0.41		1.00									
Verify		0.04	200	/S.0					-0.35		0.40									
Psi Blast	6.4e - 33	1,3e-31	00	4.8e-32		4.8e-32			3.2e-28		1.30-37							1.3e-37		
END AA	238	237	027	427		453			488		126							921		
STAR T AA	83	96		3/1		372			333		4							'n		
CHAI N ID	Ą	A		<		∢			¥		A							<		
PDB ID	2gli	2gli		uan		lalh			laIh		Ipno						1	lbuo		
SEQ No. 15	1859	1859	0,00	1890		1860			1860		1860							1860		

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PDB annotation	CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA NTERACTION PROTEIN DESIGN 2	CRYSTAL STRUCTURE, COMPLEX	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	NTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (TRANSCRIPTION	REGULATION/DNA) TFIIIA; 5S	GENE; NMR, TFIIIA, PROTEIN, DNA,	TRANSCRIPTION FACTOR, 5S RNA 2	GENE, DNA BINDING PROTEIN,	ZINC FINGER, COMPLEX 3	TRANSCRIPTION	REGULATION/DNA)	COMPLEX (TRANSCRIPTION	VET ATTOMONIA VOLUMENT TO THE
	ESE	0 5	12	8	8	E	Ξ	SE	3	E	Z	S	2	8	E	Ξ	8	-		2	B	E	Œ	ZII	Ě	RE	CO	Ď,
Coumpound		DNA; CHAIN: A, B, D, E;	PROTEIN CHAIN: C F G	, , , , , , , , , , , , , , , , , , ,	DNA: CHAIN: A. B. D. E.	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;		DNA: CHAIN: A. B. D. E.	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;			DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;	,		TRANSCRIPTION FACTOR IIIA;	CHAIN: A; 5S RNA GENE;	CHAIN: B, F;						TFIIIA; CHAIN: A, D; 5S	DIBOCOMAY DATA CRAIM.
SEQFOL D score									62.29																			
PMF		60.0			1.00									0.71					0.23								0.11	
Verify		-0.44			0.14									-0.16					-0.48								-0.38	_
Psi Blast		1.6e-47			1.3e-50				1.3e-50					3.2e-47					3.2e-19								1.6e-31	_
END		423			452				452					488					488							_	490	
STAR T AA		336			370				370					398					336								371	
CHAI N ID		၁			o				C					ပ				-	٧								A	
rob ID		Imey			Imey				Imey					Imey					9								<u>1</u> 1	_
SEQ NO. ID		1860			1860				1860					1860				0000	1860								1860	

	N, ZINC	A ANG I; M, ZINC 2 TEIN	A'ANG 1; N, ZINC 2 TEIN	ANG 1; N, ZINC 2 TEIN	R GLI; X (DNA-	R GLI;
PDB annotation	REGULATION/DNA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN	COMPLEX (TRANSCREPTION REGULATION/DNA) TYNG-YANG I; RRANSCREPTION INITIATION, INITIATION, INITIATION, RECOGNITION, 3 COMPLEX (TRANSCREPTION) TRANSCREPTION RECOGNITION, 3 COMPLEX (TRANSCREPTION)	COMPLEX (TRANSCRIPTION EL REGULATION/ONA) YING-YANG I; REAUGLATION/ONA) YING-YANG I; RRANSCRIPTION INITIATION, TRANSCRIPTION INITIATION ELEMENT, YY1, ZINC2 PRINCER PROTEIN DIAA-PROTEIN RECOGNITION, 3 COMPLEX RECOGNITION, 3 COMPLEX RECOGNITION, 3 COMPLEX RECULATION/DIA	COMPLEX (TRANSCRIPTION REGULATIONA) YING-YANG I; TRANSCRIPTION INTITATION, TRANSCRIPTION INTITATION, TRANSCRIPTION INTITATION, TRANSCRIPTION INTO REGULATION INTO REGULATION REGULATION INTO REGULATION REGULATION REGULATION	COMPLEX (DNA-BINDING PROTEINDNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI:
	X L L	OMPHERCE	OKHELKCK	OKHILKCK		
Coumpound		YYI; CHANN; C; ADENO- ASSOCIATED VIRUS PS INITIATOR ELEMENT DNA; CHAIN; A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS PS INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHAIN; C; ADBNO- ASOCIATIED VIRUS PS INITIATOR ELEMENT DNA; CHAIN: A, B;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;
SEQFOL D score						
PMF		0.92	0.89	0.10	-0.20	0.07
Verify		-0.05	-0.03	-0.08	0.05	0.10
Psi Blast		1.1e-32	6.4e-34	4.8e-24	1.6e-09	6.4e-34
END		448	488	493	313	452
STAR T AA		344	375	406	224	319
CHAI		၁	υ	υ	A	Ą
PDB		Iubd	Jubd	Jubd	2gli	2gli
SEQ No:		0981	1860	1860	0981	0981

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PDB annotation	GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)	REPLICATION DNA NUCLEOTIDE	EXCISION REPAIR, UVRABC,	HYPERTHERMOSTABLE PROTEIN	HYDROLASE UVRB; MULTIDOMAIN PROTEIN	HYDROLASE UVRB; MULTIDOMAIN PROTEIN	GENE REGULATION APO PROTEIN	TRANSLATION YEAST INITIATION	FACTOR 4A, EIF4A; HELICASE, INITIATION FACTOR 4A, DEAD-BOX PROTEIN	TRANSLATION EUKARYOTIC INITIATION FACTOR 4A; 1F4A, HELICASE, DEAD-BOX PROTEIN	TRANSLATION EUKARYOTIC INITIATION PACTOR 40; 1F4A, HELICASE, DEAD-BOX PROTEIN		TRANSPORT PROTEIN TC4; GTPASE, NUCLEAR TRANSPORT, TRANSPORT PROTEIN	TRANSPORT PROTEIN TC4, GTPASE, NUCLEAR TRANSPORT, TRANSPORT PROTEIN
Coumpound		ZINC FINGER PROTEIN GLJI; CHAIN: A; DNA; CHAIN: C, D;	DNA NUCLEOTIDE EXCISION	REPAIR ENZYME UVRB;	CHAIN: A,	EXCINUCLEASE ABC SUBUNIT B; CHAIN: A;	EXCINUCLEASE ABC SUBUNIT B: CHAIN: A:	EXCINUCLEASE UVRABC COMPONENT ITYRB: CHAIN: A:	EUKARYOTIC INITIATION	FACTOR 4A; CHAIN: A;	YEAST INITIATION FACTOR 4A; CHAIN: A, B;	YEAST INITIATION FACTOR 4A; CHAIN: A, B;		GTP-BINDING PROTEIN RAN; CHAIN: A, B;	GTP-BINDING PROTEIN RAN; CHAIN: A, B;
SEQFOL D score															113.24
PMF		0.11	0.18			0.46	0.39	0.24	0.55		-0.14	0.43		00.1	
Verify score		-0.09	0.13			0.05	-0.11	-0.27	0.23		0.09	0.06		0.35	
Psi Blast		1.6e-34	1.6e-13			1.6e-13	1.4e-07	6.4e-17	9.6e-39		4.8e-43	3.2e-91		7.5e-64	7.5e-64
END		490	630			630	995	859	029		321	670		211	217
STAR T AA		344	470			470	538	457	208		105	313		14	15
CHAI N ID		4	V			V	¥.	∀	A		<	ш		¥	<
PDB ID		2gli	1040			1d2m	1d2m	x6p1	1fuk		1gm	ng ₁		1byu	lbyu
SEQ NO:		1860	1861			1981	1861	1861	1861		1861	1861		1862	1862

PDB annotation	TRANSPORT PROTEIN TC4; GTPASE, NUCLEAR TRANSPORT, TRANSPORT PROTEIN	TRANSPORT PROTEIN TC4; GTPASE, NUCLEAR TRANSPORT, TRANSPORT PROTEIN	SIGNALING PROTEIN GTP-BINDING PROTEINS, PROTEIN-PROTEIN COMPLEX, EFFECTORS	SIGNALING PROTEIN GTP-BINDING PROTEINS, PROTEIN-PROTEIN COMPLEX, EFFECTORS	SIGNALING PROTEIN, GTP HYDROLYSIS, KINETIC CRYSTALLOGRAPHY, 2 SIGNALING PROTEIN	SIGNALING PROTEIN G PROTEIN, GTP HYDROLYSIS, KINETIC CRYSTALLOGRAPHY, 2 SIGNALING PROTEIN	SIGNALING PROTEIN PROTEIN- PROTEIN COMPLEX, ANTIPARALLEL COILED-COIL	ENDOCYTOSIS/EXOCYTOSIS G- PROTEIN, GTPASE, RAB6, VESICULAR TRAFFICKING	ENIDOCYTOSIS/EXOCYTOSIS G PROTEIN, VESICULAR TRAFFIC, GTP HYDROLYSIS, YPT/RAB 2 PROTEIN, ENDOCYTOSIS,
Coumpound	GTP-BINDING PROTEIN RAN; CHAIN: A, B;	GTP-BINDING PROTEIN RAN; CHAIN: A, B;	RAS-RELATED PROTEIN RAP- 1A; CHAIN: A; PROTO- ONKOGENE SERINE/THREONINE PROTEIN KINASE CHAIN: B:	RAS-RELATED PROTEIN RAP- 1A; CHAIN: A; PROTO- ONKOGENE SPRING/THREONINE PROTEIN KINASE CHAIN: B;	TRANSFORMING PROTEIN P21/H-RAS-1; CHAIN: A;	TRANSFORMING PROTEIN P21/H-RAS-1; CHAIN: A;	HIS-TAGGED TRANSFORMING PROTEIN RHOA(0-181); CHAIN: A: PKN; CHAIN; B:	RÁB6 GTPASE; CHAIN: A;	GTP-BINDING PROTBIN YPT51; CHAIN: A;
SEQFOL D score		109.68		102.67		98.76	95.76		
PMF score	1.00		00:1		1.00			1.00	1.00
Verify score	0.44		0.51		0.65			0.56	0.68
Psi Blast	1.3e-65	1.3e-65	8e-65	8e-65	6.4e-64	6.4e-64	3.2e-58	3.2e-62	9.6e-60
END	211	215	181	181	182	182	182	179	179
STAR	6	6	16	17	17	17	- 61	81	18
CHAI N ID	В	В	∢	<	4	¥	¥	A	∢
EDB EDB	1byu	1byu	lcly	lcly	letq	letq	lexz	1450	lek0
SEQ NO:	7981	1862	1862	1862	1862	1862	1862	1862	1862

PDB CHAI STAR END Psi Blast V ID NID TAA AA s	STAR END Psi Blast TAA AA	END Psi Blast	END Psi Blast		> %	Verify	PIMF	SEQFOL D score	Coumpound	PDB annotation
										HYDROLASE
1ibr A 17 187 3e-60	17 187	187		3e-60				113.50	RAN; CHAIN: A, C; IMPORTIN BETA SUBUNIT; CHAIN: B, D;	SMALL GTPASE KARYOPHERIN BETA, P95 SMALL GTPASE, NIICI FAP TR ANSPORT BECEPTOR
libr A 18 186 3e-60 0.80	18 3e-60	186 3e-60	3e-60		0.80		1.00		RAN; CHAIN: A, C; IMPORTIN BETA SUBUNIT; CHAIN: B, D;	SMALL GTPASE KARYOPHERIN BETA, P95 SMALL GTPASE, NICT FAR TRANSPORT RECEPTOR
1kao 17 182 9.6e-59	182	182		9.6e-59				98.96	RAP2A; CHAIN: NULL;	GTP-BINDING PROTEIN GTP- BINDING PROTEIN, SMALL G PROTEIN, RAPZ, GDP, RAS
Iтр C 15 198 1.4e-60	15 198	861		1.4c-60				114.45	RAN; CHAIN: A, C; NUCLEAR PORE COMPLEX PROTEIN NUP358; CHAIN: B, D;	COMPLEX (SMÁ11 GTPASROUCLEAR PROTEIN) COMPLEX (SMALL GTPASEAUCLEAR PROTEIN), SMALL GTPASE, 2 NUCLEAR TRANSORT
1rrp C 16 193 1.4c-60 0.45	16 193 1.4e-60	193 1.46-60	1.4c-60		0.45		1.00		RAN; CHAIN: A, C; NUCLEAR PORE COMPLEX PROTEIN NUP358; CHAIN: B, D;	COMPLEX (SMALL GTPASENUCLEAR ROTEIN) COMPLEX (SMALL GTPASENUCLEAR PROTEIN), SMALL GTPASE, 2 NUCLEAR TRANSPORT
1k4 B 19 180 4.8e-55	180	180		4.8e-55				87.88	PSO-RHOGAP; CHAIN: A; TRANSPORMING PROTEIN RHOA; CHAIN: B;	COMPLEX(GTPASE ACTIVATA/PROTO-OCOGENE) GTPASE-ACTIVATING PROTEIN RHOGAP; COMPLEX (GTPASE ACTIVATION/PROTO-ONCOGENE) GTPASE 2 TRANSITION STATE GAP
12bd A 12 187 4.8e-69	12 187	187		4.8e-69				130.15	RAB-3A; CHAIN: A; RABPHLIN-3A; CHAIN: B;	COMPLEX (GTP- BINDINGEFECTOR) KAS-RELATED PROTEIN RABJA, COMPLEX (GTP- BINDINGEFECTOR), G PROTEIN, EFFECTOR, RABODE, S SYNAPTIC EXOCYTOSIS, RAB PROTEIN,

PDB annotation	RAB3A, RABPHILIN	COMPLEX (GIP- BINDINGEPFECTOR) RAS-RELATED BINDINGEPFECTOR, ORAPLEX (GIP- BINDINGEPFECTOR, OR PROTEIN, EFFECTOR, RABCR, 2 SYNAPTIC EXOCYTORIS, RAB PROTEIN, RARAR A RABPHIN D	HYDROLASE G PROTEIN, VESICULAR TRAFFICKING, GTP HYDROLYSIS, RAB 2 PROTEIN, BUROTRANSMITTER RELEASE, HYDROLASE	HYDROLASE G PROTEIN, VESICULAR TRAFFICKING, GTP HYDROLYSIS, RAB 2 PROTEIN, NEUROTRANSMITTER RELEASE, HYDROLASE	COMPLEX (NUCLEAR PROTEIN/RNA), COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP, RIBONUCLEOPROTEIN		GENE REGULATION/RNA POLY(A) BINDING PROTEIN I, PABP I; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	GENE REGULATION/RNA POLY(A)
Coumpound		RAB-3A; CHAIN: A; RABPHILIN-3A; CHAIN: B;	RAB3A; CHAIN: A;	RAB3A; CHAIN: A;	U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'- R(P*GP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP	POLYDENYLATE BINDING PROTENT I; CHAIN: A, B, C, D, B, F, G, H; RN4 (5'- R(*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP; CHAIN: M, N, O, P, O, R, S, T,	POLYDENYLATE BINDING
SEQFOL D score				145.01				
PMF		8:	1.00		0.52	0.43	0.57	0.43
Verify		0.65	0.78		0.40	90.08	0.47	0.54
Psi Blast		4.8e-69	8e-70	8e-70	7.5e-07	3e-07	7.5e-07	7.5e-07
END		185	182	182	202	207	205	199
STAR T AA		14	13	13	135	138	138	136
CHAI N ID		∀	∢	V V	В	¥	∢	ţĿ,
PDB ID		1zbd	3rab	3rab	la9n	1b7f	fevj	lcvj
SEQ NO:		1862	1862	1862	1864	1864	1864	1864

PDB annotation	BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	STRUCTURAL PROTEIN PROTEIN C23; RNP, RBD, RRM, RNA BINDING DOMAIN, NUCLEOLUS		RIBONUCLEOPROTEIN PTB, PTB- C198, IETEROGENEOUS NUCLEAR POLYPYRIBIDINE TRACT BINDING PROTEIN, RNP, RNA, SPICING, 2 TRANSLATION	NUCLEAR PROTEIN UI SNRNP A PROTEIN; RNA BINDING DOMAIN, NUCLEAR PROTEIN	COMPLEA (RIBONUCLEOPROTEINDNA) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEINDNA), HEITEROGENBOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2
Commound	PROTEIN I; CHAIN: A, B, C, D, E, F, G, H, RNA (5*- R(*Ap*Ap*Ap*Ap*Ap*Ap*Ap* AP*Ap*Ap*Ap*Ap*Ap* O, R, S, T; O, R, S, T,	NUCLEOLIN RBD1; CHAIN: A;	INDONICLEOPROTEIN PROJECTEN PROMULI SWALL NUCLEAR RIBONICLEOPROTEIN (SRNNP U) INRC 3 (W-TERMILIAL ACADERNI, PERSIDIOES 1-95) MUTANY WITH GLY 8S INRC 5 INRC 5	POLYPYRIMIDINE TRACT- BINDING PROTEIN, CHAIN: A;	I UI SMALL NUCLEAR RIBONUCLEOPROTEIN A; CHAIN: NULL;	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A1 IZ-NUCLEOTIDE SINGILE-STRANDED TELOMETRIC DINA; CHAIN: B;	SEX-LETHAL, CHAIN: A, B, C,
SEQFOL D score							
PMF		0.21	0.99	0.15	0.43	0.95	0.48
Verify score		0.48	0.13	0.20	0.05	0.32	0.38
Psi Blast		60-07	1e-08	6e-07	20-09	7.5e-07	3e-07
END		961	195	961	195	961	207
STAR T AA		136	135	88	136	138	138
CHAI N ID		<	m	A		A	٧
FDB EDB		107	Inc	1qm9	2ula	2up1	3sxl
SEQ NO ID		1864	1864	1864	1864	1864	1864

	-n (1)	_		_			_		
PDB annotation	SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION				COMPLEX (TRANSCRIPTION FACTORDNA) COMPLEX (TRANSCRIPTION FACTOR/DNA), TRANSCRIPTION FACTOR, 2 DNA- BINDING PROTEIN	COMPLEX (TRANSCRIPTION FACTORDNA) COMPLEX (TRANSCRIPTION FACTOR/DNA), TRANSCRIPTION FACTOR, 2 DNA- BINDING PROTEIN		COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (NHHBITOR/NUCLEASE), COMPLEX (NHHBITOR/NUCLEASE), MOLECULAR RECOGNITION, BETTOPE MAPPING, LEUCINE-RICH 3 REPAATS	COMPLEX (INHIBITORNUCLEASE) COMPLEX (INHIBITORAUCLEASE), COMPLEX (RIANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH
Coumpound			LIGASE(SYNTHETASE) SERYI TRNA SYNTHETASE (B.C.6.11.11) (SERINE-TRNA LIGASE) 1SES 3 COMPLEXED WITH SERYIHYDROXAMATE- AMP 1SES 4		T PROTEIN; CHAIN: A, B; DNA; CHAIN: C, D;	T PROTEIN; CHAIN: A, B; DNA; CHAIN: C, D;		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	RIBONUCLEASE INHIBITOR; CHAIN: A, D, ANGIOGENIN; CHAIN: B, E;
SEQFOL D score									
PMF			0.01		0.60	0.47		0.43	09.0
Verify score			-0.21		-0.88 8	-0.90		0.30	0.15
Psi Blast			3.2e-05		1.6e-21	1.2e-37		8e-08	1.4e-08
END			542		94	96		350	338
STAR T AA			439		_	-		183	209
CHAI N ID			Ą		∢	¥		¥	Ą
PDB TD			Iscs		Ixbr	lxbr		la4y	la4y
SEQ No:			1865		1867	1867		1870	1870

PDB annotation	3 REPEATS	COMPLEX (INHIBITORANUCIEASE) COMPLEX (INHIBITORANUCIEASE),	MOLECULAR RECOGNITION,	EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION	RNA BINDING PROTEIN TAP (NFXI);	RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-	REPEAT 2 (LRR)	RNA BINDING PROTEIN TAP (NFX1);	OR RRM) AND LEUCINE-RICH-	LIGASE CYCLIN A/CDK2.	ASSOCIATED PROTEIN P45; CYCLIN	A/CDK2-ASSOCIATED PROTEIN P 19;	SKP1, SKP2, F-BOX, LRR, LEUCINE-	RICH REPEAT, SCF, UBIQUITIN, 2 E3 TIBIOTITIN PROTEIN LIGASE	LIGASE CYCLIN A/CDK2-	ASSOCIATED P45; CYCLIN A/CDK2-	ASSOCIATED P19; SKP1, SKP2, F-	BOX, LRRS, LEUCINE-RICH	UBIOUITIN PROTEIN LIGASE	TRANSCRIPTION RNAIP; RANGAP;
Coumpound	3	RIBONUCLEASE INHIBITOR; CO		EE 33	INTERNALIN B; CHAIN: A; CI	INTERNALIN B; CHAIN: A; CI	NUCLEAR RNA EXPORT RI	FACTOR 1; CHAIN: A, B; RI	RI	NUCLEAR RNA EXPORT		SKP2: CHAIN: A C E G L K M LT	PI; CHAIN: B, D, F, H, J, L,	£ 5.	S	3 1	SKP2; CHAIN: A, C; SKP1;		~	BO	25	GTPASE-ACTIVATING TI
SEQFOL D score																						
PMF		0.25			0.12	0.25	0.03			0.00		0.51					0.72					0.27
Verify score		0.14			0.40	-0.10	0.03			-0.01		0.45					0.22					60.0
Psi Blast		3e-06			8e-07	0.00096	1.Ie-06			1.1e-06		1.1e-46					4.8e-36					0.00064
END		373			333	354	306			306		349					349					347
STAR T AA		209			961	222	193			193		128					128					248
CHAI N ID		A			A	٧	Ą			м		V					A					Ą
PDB ID		la4y			10p1	1d0b	10J1			Ig.		Ifqv					1fs2					lyrg
SEQ ID NO:		1870			1870	0281	1870			1870		1870					1870					1870

CHAI STAR EN NID TAA A			END	Psi Blast	Verify	PMF	SEQFOL D score	Coumpound	PDB annotation
								PROJEINKANI_SCHPO; CHAIN: A, B;	GIPAGA-CITACIUN FROLBIN PROTEN, GAP, RNAIP, RANGAP, LRR, LEGUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, MEROHEDRAL TWINNING,
209 338	338			3.2e-09	-0.03	0.71		RIBONÚCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASEANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
. 168 291	291		*	4.8e-10	0.08	-0.03		G-PROTEIN COUPLED RECEPTOR KINASE 2; CHAIN: NULL;	ARABERAKS GERZ, BETA- ARABERREGIC RECEPTOR KINASE I, HOMOLGY DOMANN PHODANN HOMOLGY DOMANN PHODANN ESTA-CANAR ENERGIE RECEPTOR 3 ESTA-CANARKE ENERGE RECEPTOR 3 KINASE BETA-ARK G-PROTEIN COUPLED RECEPTOR KINASE (GRK-
172 271 8	271			8e-12	61.0	96.0		BETA-SPECTRIN; 1BTN 4 CHAIN: NULL; 1BTN 5	SIGNAL TRANSDUCTION PROTEIN
182 264		264		1.5e-05	0.22	0.21		BETA-SPECTRIN; IDRO 6 CHAIN: NUIL; IDRO 7	CYTOSKELETON
A 186 271	271			4.8e-10	0.13	0.11		SIGNAL TRANSDUCTION PROTEIN DYNAMIN (PLECKSTRIN HOMOLOGY DOMAIN) (DYNPH) IDYN 3	
A 149 464	464			1.6e-58	0.05	0.53		MOESIN; CHAIN: A, B; MOESIN; CHAIN: C, D;	MEMBRANE PROTEIN CRYSTAL STRUCTURE, MEMBRANE, FERM DOMAIN, TAIL DOMAIN

Coumpound PDB annotation	R OF SIGNALING PROTEIN DAPPI, PHISH, DSINE AND 3- BAARZ PLECKETRIN, 3- PHOSPHORNSTITIDES, INGSTOL, TETRA KISHOSHARI Z SIGNAL TRANSDICTION PROTEIN, ADAPTOR PROTEIN		A; SIGNALING PROTEIN ARF! GUANINE NUCLEOTIDE EXCHANGE FACTOR AND PH DOMAIN	IN: A; CELL ADHESION 3 SUBDOMAINS, CYTOSKELETON, CELL ADHESION	PLECKSTRIN (A-TERMINAL PLECKSTRIN (A-TERMINAL PLECKSTRIN (A) OND (A) O	1-SOUROPYLAMIATE DEHYDROGENASE, CHAIN: A) DEAVBOOKTIANE A) DEAVBOOKTAKE B) DEAVBOOKTATING DEAVBOOKTATING DEAVBOOKTATING DEAVBOOKTATING DEAVBOOKTATING DEAVBOOKTATING DEAVBOOKTATING DEAVBOOKTATING DEAVBOOKTATING DEAVBOOKTA	
SEQFOL Coun	DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3- CHAIN: A;	DUAL ADAPTOR OF PHOSPHOTYROSINE AND 3- CHAIN: A;	GRP1; CHAIN: A;	RADIXIN; CHAIN: A;	PHOSPHORYLATION PLECKSTRIN (N-TERMINAL PLECKSTRIN HOWOLOGY DOMANIY MUTTANT PIES 3 WITH LEU GLU (HIS) & WITH LEU GLU (HIS) & DOES TO THE C TERMINUS IPLS 4 (INS(OIG-LEHIHHHHIN) (NM 25 STRUCTNES) IPLS 5		
PMF SE score D	Q.	<u>o</u>	22	=	Q	69.11	
Verify P	08.0	69.0	90.0	10.01	0.09	-	
	0.31	0.14	0.49	-0.01	4. 1.0	-	
Psi Blast	3.2e-17	3.2e-17	4.8c-18	3.2e-58	1,46-14	0	
END	269	269	272	464	285	390	
STAR T AA	170	170	172	134	691	17	
CHAI N ID	A	⋖	۷	A		<	
908 CI	Ifao	108	Ifgy	1gc7	īpis	1a05	
SEQ NO.	1871	1871	1871	1871	1871	1872	

PDB annotation	DECARBOXYLATING DEHYDROGENASE, LEUCINE 2 BIOSYNTHESIS	OXIDOREDUCTASE OXALOSUCCINATE DECARBOXTLASE, IDH, OXIDOSEDUCTASE, IDH, CHOH(D)), NADP, PHOSPHOYTA, ATTON, 2 GLYOXYLATE BYPASS	OXADOSDUCIASE OXALOSUCCINATE BECARBOXYLASE, IDH, OXTDOSDUCTASE (NADKA)- CHOH(D)), NADP, PHOSPHOSTA, ATTE NYPASS GI XOXYLATTE NYPASS	OXIDOREDUCTASE IPMDH, IMDH; OXIDOREDUCTASE, DEHYDROGENASE, NAD- DEPENDANT ENZYME, 2 LEUCINE BIOSYVITHETIC PATTHWAY	OXIDOREDUCTASE IPMDH, IMDH; OXIDOREDUCTASE, DEHYDROGENASE, NAD- DEPENDANT ENZYME, 2 LEUCINE BIOSYNTHETIC PATHWAY	OXIDOREDUCTASE IPMDH, IMDH; OXIDOREDUCTASE, DEPTYDROORDASE, LEUCINE BIOSYNTHETIC PATHWAY, 2 NAD- DEPENDANT ENZYME	OXIDOREDUCTASE IPMDH, IMDH; OXIDOREDUCTASE,
Coumpound	Ď.	ISOCITRATE DEHYDROGENASE; CHAIN: NULL;	ISOCITRATE DEHYDROGENASE; CHAIN: NULL;	3-ISOPROPYLMALATE DEH YDROGENASE; CHAIN: A, B;	3-ISOPROPYLMALATE DEHYDROGENASE; CHAIN: A, B;	3-ISOPROPYLMALATE DEHYDROGENASE; CHAIN: A, B;	3-ISOPROPYLMALATE DEHYDROGENASE; CHAIN: A,
SEQFOL D score			62.58	63.70		60.42	
PMF		0.60			0.41		9.65
Verify		0.01			0.04		-0.04
Psi Blast		0	0	0	0	0	0
END AA		387	387	382	389	382	389
STAR		m	7	-	_	_	_
CHAI				<	V	V	٧
PDB		lai2	lai2	lcm7	1cm7	lonz	Icnz
SEQ NO.		1872	1872	1872	1872	1872	1872

		, ,				,		
DEHYDROGENASE, LEUCINE BIOSYNTHETIC PATHWAY, 2 NAD- DEPENDANT ENZYME	OXIDOREDUCTASE IPMDH, 1IDM 7 CHIMERA 1IDM 20	OXIDOREDUCTASE IPMDH; 1IDM 7 CHIMERA 1IDM 20	OXIDOREDUCTASE IPMDH, IMDH; 1XAC 10 OXIDOREDUCTASE, CHIMERA 1XAC 21	OXIDOREDUCTASE IPMDH, IMDH; IXAC 10 OXIDOREDUCTASE, CHIMERA IXAC 21	OXIDOREDUCTASE OXIDOREDUCTASE, 3- ISOPROPYLAALATE DEHYDROGENASE, LEUCINE 2 BIOSYNTHESIS, MODERATE THERMOPHILE	OXIDOREDUCTASE OXIDOREDUCTASE, 3- ISOPROPYLAALATE DEHVDROGENASE, LEUCINE 2 BRIOSYNTHESIS, MODERATE THERMOPHILE	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT	COMPLEX (TRANSCRIPTION
B;	3-ISOPROPYLMALATE DEHYDROGENASE; 11DM 5 CHAIN; NULL; 11DM 6	3-ISOPROPYLMALATE DEHYDROGENASE; 11DM 5 CHAIN; NULL; 11DM 6	3-ISOPROPYLMALATE DEHYDROGENASE ZTZM6T S82R; IXAC 8 CHAIN: NULL; IXAC 9	3-ISOPROPYLMALATE DEHYDROGENASE ZTZMGT S82R; IXAC 8 CHAIN; NULL; IXAC 9	3-ISOPROPYLMALATE DEHYDROGENASE, CHAIN: A, B;	3-ISOPROPYLMALATE DEHYDROGENASE, CHAIN: A, B;	TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	GA BINDING PROTEIN ALPHA; COMPLEX (TRANSCRIPTION
	54.18		50.68			68.62		
		0.42		0.46	0.57		0.51	0.22
		90.0		9.04	-0.03		0.44	0.11
	4.8e-95	4.8e-95	1.6e-96	1.6e-96 ·	0	0	1.6e-23	4.8e-36
	366	387	366	387	387	388	125	156
	42	6	42	6	9	9	10	10
					¥	4		В
	lidm	lidm	lxac	Ixac	2ayq	2ayq	la5e	lawc
	1872	1872	1872	1872	1872	1872	1873	1873
		Bs Bs Bs Bs Bs Bs Bs Bs	B; B; B; B; B; B; B; B;	Bi Bi Bi Bi Bi Bi Bi Bi	Bi Bi Bi Bi Bi Bi Bi Bi	Hidm 42 366 48e-95 5418 3-1SOPROPYLAMAATE	Hidm	Hidam 42 366 48e-95 54118 3-1SOPROPYLAMAATE Hidam 9 387 48e-95 0.06 0.42 DEHTYDROCHEARSE; IDM 5 Hade 42 366 1.6e-96 0.66 0.42 DEHTYDROCHEARSE; IDM 5 Hade 42 366 1.6e-96 0.66 0.46 DEHTYDROCHEARSE; IDM 5 Hade 9 387 1.6e-96 0.04 DEHTYDROCHEARSE; IDM 5 Hade 9 387 1.6e-96 0.04 DEHTYDROCHEARSE; IDM 5 Hade 9 387 0 0.04 DEHTYDROCHEARSE; CHAIR; A, B,

	σź	rî Zî		T	щ	Ι .
PDB annotation	REGULATION/DNA) GABPALPHA; GABPBETA; COMPLEX (TRANSCRIPTION REGULATION/DNA, DNA-BINDING, 2 NUCLEAR PROTEN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 PACTOR	COMPLEX (TRANSCRIPTION REGULATION/NOMA) GABRALPHA; GABRETA; COMPLEX (TRANSCRIPTION TREGULATION/DNA), DNA-BINDING, BEGULATION/DNA), DNA-BINDING, ANCYGEN REPERE, ANCYGEN REPERE, ANCYGEN REPERE, ANCYGEN REPERED, TRANSCRIPTION 5 FACTOR.	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	ONCOGENCY, PLANSERATI- ONCOGENCY, DIAMERA, MTSI, CYCLIN DEFENDENT KINAGE, CYCLIN DEFENDENT KINAGE, CYCLIN DEFENDENT KINAGE, CYCLIN DEFENDENT TINAGE, CYCLIA MILTIPLE TUMOR SUPPRESSOR, 3 MINUTIPLE ONCOGENCY TO COMPERATION	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL.
Coumpound	CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, B;	GA BINDING PROTEIN ALPHA; GARIN A; GA BINDING PROTEIN BETA I; CHAIN: B; DNA; CHAIN: D, B;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19NK4D CDK4/6 INHIBITOR; CHAIN: NULL;	CCIAN-DEPENDENT KINASE 6; CHARI: A: MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;
SEQFOL D score						
PMF		1.00	0.11	96'0	0.62	0.15
Verify score		0.43	0.05	0.22	0.52	0.18
Psi Blast		6.4e-33	3.2e-32	1.1e-23	86-24	80-33
END		125	157	128	125	157
STAR T AA		2	13	6	10	13
CHAI N ID		ш			В	В
PDB ID		lawc	1bd8	1bd8	1617	Ibix
SEQ ID NO:		1873	1873	1873	1873	1873

											_	_							_	_	_		
PDB annotation	ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN/CYCT IN PREPARENT	FROTEIN, CTCLIN-DEFENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX	HORMONE/GROWTH FACTOR P18-	INK4C; CELL CYCLE INHIBITOR,	CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR	HORMONE/GROWTH FACTOR P18-	INK4C; CELL CYCLE INHIBITOR,	CYCLIN-2 DEPENDENT KINASE.	HORMONE/GROWTH FACTOR	SIGNALING PROTEIN HELIX-TURN-	CELL CYCLE INHIBITOR PIR.	INK4C(INK6); CELL CYCLE	INHIBITOR, P18-INK4C(INK6),	ANKYRIN REPEAT, 2 CDK 4/6	CELL CYCLE INHIBITOR P18-	INK4C(INK6); CELL CYCLE	INHIBITOR, P18-INK4C(INK6),	ANKYRIN REPEAT, 2 CDK 4/6	INHIBITOR	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT	COMPLEX (TRANSCRIPTION	REGVANK REPEAT) COMPLEX
Coumpound		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; PI9INK4D; CHAIN:	G	CYCLIN-DEPENDENT KINASE	6 INHIBITOR; CHAIN: A;		CYCLIN-DEPENDENT KINASE	6 INHIBITOR; CHAIN: A;			CYCLIN-DEPENDENT KINASE	CYCLIN-DEPENDENT KINASE	6 INHIBITOR; CHAIN: A. B:			CYCLIN-DEPENDENT KINASE	6 INHIBITOR; CHAIN: A, B;				MYOTROPHIN; CHAIN: NULL	NF-KAPPA-B P65; CHAIN: A, C;	NF-KAPPA-B P50; CHAIN: B, D;
SEQFOL D score																							
PMF		96.0		0.71			0.55				0.49	0 60	2			0.74					0.64	0.45	
Verify score		0.42		91.0			0.15				0.05	0.23]			0.14					0.21	0.02	
Psi Blast		1.6e-22		6.4e-34			4.8e-27				3.2e-24	6 46-34				1.6e-26		-			1.3e-24	3.2e-40	
END AA		128		153			130				131	153	}			129					127	212	
STAR T AA		3		10			2				10	10	:			2					=	4	
CHAI N ID		m		4			Ą				∢	V	:			A					,	11	
rog ID		1blx		1bu9			1bu9				1d9s	lih				lihb					Imyo	jul j	
SEQ No no		1873		1873			1873				1873	1873				1873					1873	1873	

			,											
PDB annotation	(TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF	COMPLEX (KINASE/ANTI- ONCOGENE) CDK6; P16INK4A, MTS1; CYCLIN DEPENDENT	KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4. CELL CYCLE, MULTIPLE	TUMOR SUPPRESSOR, 3 MTSI, COMPLEX (KINASE/ANTI-	COMPLEX (KINASE/ANTI-	ONCOGENE) CDK6; P16INK4A, MTS1: CYCLIN DEPENDENT	KINASE, CYCLIN DEPENDENT	CDK, INK4, CELL CYCLE, MULTIPLE	TOMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI-	ONCOGENE) HEADER	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR
Coumpound	I-KAPPA-B-ALPHA; CHAIN: E, P;	TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	P19INK4D CDX4/6 INHIBITOR; CHAIN: NULL;	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN:	á,		CYCLIN-DEPENDENT KINASE	6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR: CHAIN:	B,				CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN:
SEQFOL D score														
PMF		0.81	0.31	10:0	99.0			00:0						0.31
Verify score		0.03	0.03	-0.04	0.18			0.15	·					60:0
Psi Blast		3.2e-16	3.2e-27	1.4e-15	3.2e-17			I.4e-17						3.2e-25
END AA		120	153	120	120			153						153
STAR T AA		9	13	2	10			52						13
CHAI N ID					В			В						Д
PDB		laSe	1bd8	8Pq1	1bi7			1bi7						zigi.
SEQ ID NO:		1874	1874	1874	1874			1874						1874

PDB annotation	KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)			ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)	HORMONE/GROWTH FACTOR P18-	INK4C; CELL CYCLE INHIBITOR,	CYCLIN-2 DEPENDENT KINASE	HORMONE/GROWTH FACTOR	HORMONE/GROWTH FACTOR P18-	INK4C; CELL CYCLE INHIBITOR,	P18INK4C, TUMOR, SUPPRESSOR,	CYCLIN- 2 DEPENDENT KINASE,	HORMONE/GROWTH FACTOR	HORMONE/GROWTH FACTOR P18-	INK4C; CELL CYCLE INHIBITOR,	P18INK4C, TUMOR, SUPPRESSOR,	CYCLIN- 2 DEPENDENT KINASE,	HORMONE/GROWTH FACTOR	SIGNALING PROTEIN HELIX-TURN-	HELIX, ANKYRIN REPEAT	METAL BINDING PROTEIN ZINC-	BINDING MODULE, ANKYRIN	REPEATS, METAL BINDING	PROTEIN	CELL CYCLE INHIBITOR P18-	INK4C(INK6); CELL CYCLE	INHIBITOR, P18-INK4C(INK6),	ANKYKIN KEPEA1, 2 CUK 4/6
Coumpound		6; CHAIN: A; P19INK4D; CHAIN:	ėď		CYCLIN-DEPENDENT KINASE	6 INHIBITOR; CHAIN: A;			CYCLIN-DEPENDENT KINASE	6 INHIBITOR; CHAIN: A;				CYCLIN-DEPENDENT KINASE	6 INHIBITOR; CHAIN: A;				CYCLIN-DEPENDENT KINASE	4 INHIBITOR B; CHAIN: A;	PYK2-ASSOCIATED PROTEIN	BETA; CHAIN: A;			CYCLIN-DEPENDENT KINASE	6 INHIBITOR; CHAIN: A, B;		
SEQFOL D score																												
PMF		60:0-			0.23				0.11					0.05					0.33		69.0				0.71			
Verify score		90'0			-0.15				0.04					0.01					0.28		80.0				0.40			
Psi Blast		1.6c-14			1.3e-29				1.3e-18					6.4e-28					1.ee-17		1.5e-12				4.8e-18			
END AA		120			158				125					212					120		122				124			
STAR		2			13				2					\$					10		13				2			
CHAI N ID		മ			¥				A					٧					٧		¥				<			
PDB ID		Iblx			1bu9				1bu9					1bu9					149s		ldcq				lihb			
S a S		1874			1874				1874				~	1874					1874		1874				1874			

PDB annotation	INHIBITOR CELL CYCLE INHIBITOR PIB- CELL CYCLE INHIGHOR, PIB- INHIBITOR, PIS-INK-4CINKG), ANKYKIN REPEAT, 2 CDK 446 INHIBITOR	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR. ANK-REPEAT	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR. ANK-REPEAT	ONCOGENCY AND REPEATS) PESTER, ANKTRIN REPEATS) PESTER, ANKTRIN REPEATS, SH3, PESTER, ANKTRIN REPEATS, SH3, PESTER, ANKTRIN REPEATS, SH3, MULTIGENE 2 PAMAILY, NUCLEAR, DISEASE MULTIGENS, COMPLEX (ANTI- ONCOGENCIATOR)	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA),
Commpound	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	MYOTROPHIN; CHAIN: NULL	MYOTROPHIN; CHAIN: NULL	P53; CHAIN: A; 53RP2; CHAIN: B;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE: CHAIN: B. C:	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE: CHAIN: B. C.	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX
SEQFOL D score							72.03	
PMF	0.27	0.24	0.23	0.01	99.0	0.00		0.09
Verify	-0.09	-0.17	0.30	-0.03	0.12	0.04		-0.14
Psi Blast	3.2e-27	1.1e-21	1.1e-21	4.8e-20	9.6e-26	7.5e-29	7.5e-29	1.5e-39
END AA	211	138	129	193	335	336	365	502
STAR T AA	54	=	73	99	239	243	283	395
CHAI N ID	A			α	¥	<	<	٧
PDB CI	lihb	lmyo	1myo	lycs	 laIh	lath	lalh	lalh
SEQ ID NO:	1874	1874	1874	1874	1877	1877	1877	1877

PDB annotation	ZINC FINGER, DNA-BINDING PROTEIN	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	CRYSTAL STRICTIBE, COMPLEX	ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	NTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	NTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	(ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC	FINGER, PROTEIN-DNA	INTERACTION, PROTEIN DESIGN, 2	CRYSTAL STRUCTURE, COMPLEX	ZINC FINGER/DNA)	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA
Coumpound	OLIGONUCLEOTIDE BINDING ZI SITE; CHAIN: B, C; PE		CONSENSUS ZINC FINGER FI		(2)		~	PROTEIN; CHAIN: C, F, G;		DNA; CHAIN: A, B, D, E;	ER	PROTEIN; CHAIN: C, F, G;	0			_	PROTEIN; CHAIN: C, F, G;	0			~	PROTEIN; CHAIN: C, F, G;	Ö	Z	Г	~	PROTEIN; CHAIN: C, F, G; IN	0	_	DNA; CHAIN: A, B, D, E; CO
SEQFOL D score																														98.05
PMF		90.0				0.00				0.37					0.07					0.95					1.00					
Verify		-0.16				-0.57				-0.46					-0.24					0.02					0.29					
Psi Blast		4.8e-42				1e-11				3e-26					8e-40					1.3e-39					6.4e-50					8e-51
END		563				307				335					307					335					363					364
STAR T AA		191				166				190					217					566					282					282
CHAI		၀		_		C				U					U					U					o					υ
PDB TD		lmey				lmey				lmey					lmey					1mey					lmey					Imey
SEQ NO:		1877				1877				1877					1877					1877					1877					1877

PDB annotation	G; INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGERIDNA)		G: INTERACTION PROTEIN DESIGN 2	(ZINC FINGER/DNA)	E; COMPLEX (ZINC FINGER/DNA) ZINC				IGER FINGER, PROTEIN-DNA		(ZINC FINGER (DNA)		E; COMPLEX (ZINC FINGER/DNA) ZINC			(ZINC PINGED DNA)		_	_	 (ZINC FINGER/DNA)	E; COMPLEX (ZINC FINGER/DNA) ZINC	IGER FINGER, PROTEIN-DNA		CRYSTAL STRUCTURE, COMPLEX	(ZINC FINCER/UNA)
Coumpound e	PROTEIN, CHAIN: C, F, G;	DNA; CHAIN: A, B, D, E;	PROTEIN CHAIN: C. F. G.		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER	PROTEIN; CHAIN; C, F, G;		DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	FROIDIN, CHAIN, C, F.		Tark. Criabit & D. D.	CONSENSTIS ZINC PINIGED	PROTEIN CHARLOR DO	FROIEMN, CHAMN. C, F.		DNA: CHAIN: A B. D. F.	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;		DNA; CHAIN: A, B, D, E;	CONSENSUS ZINC FINGER	PROTEIN; CHAIN: C, F, G;		
PMF SEQFOL score		0			0	_										_	2			_	0			_	
Verify Pi		0.09 1.00			0.43 1.00		1	0.28				1 00					-0.02 0.82		_		0.39 1.00				_
Psi Blast		8e-51			3.2e-51		:	1.36-50				4 00 47	4.96-4/				3e-40				3.2c-48				
END		391			419			44.				472	2				529				529				
STAR T AA		310			338		100	399		_		204	+60				422				450				
CHAI N ID		ပ			ပ			د				(ر				0				υ				
FDB TD		1mey			Imey		1	Imey				Imax	r illich				Imey				Imey				
SEQ ID NO:		_4281			1877		1000	187/				1077	101				1877				1877				

PDB CHAI STAR END Psi Blast Verify PMF ID N ID T AA AA score score	STAR END Psi Blast Verify T AA AA score	Psi Blast Verify score	Verify		PMF	SEQFOL D score	Coumpound	PDB annotation
							CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL, STRUCTURE, COMPLEX (ZINC FINGER/DNA)
Imey G 187 214 1.6c-11 -0.12 0.48	214 1.66-11 -0.12	1.6e-11 -0.12	-0.12		0.48		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA FINGER CTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
Imey G 236 263 6.4e-12 -0.05 0.52	263 6.4c-12 -0.05	6.4e-120.05	-0.05		0.52		DNA; CHAIN; A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGERJDNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1sp2 _ 190	218 9.6e-07 0.02	9.6e-07 0.02	0.02		0.09		SPIF2; CHAIN: NOLL;	ZINC FINGER TRANSCRIPTION FACTOR SP1; ZINC FINGER, TRANSCRIPTION ACTIVATION, SP1
11G A 239 335 4.8e-17 0.27 0.07	335 4.8e-17 0.27	4.8e-17 0.27	0.27		0.07		TRANSCRETTON FIG.	COMPLEX (TRANSCRIPTION REGULATION/DNA) PTHIA, 18 GENES, MAR, TPHIA, PROTEIN, DNA, TRANSCRIPTION FACTOR, 58 RNA 2 GENE, DNA BINDING PROTEIN, ZINC FINGER, COMPLEX 3 (TRANSCRIPTION
Hib A 162 316 8e-31 -0.24 0.11	316 8e-31 -0.24	86-31	-0.24		11.0		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	COMPLEX (TRANSCRIPTION REGULATIONDINA) COMPLEX (TRANSCRIPTION REGULATIONDINA), RNA POLYMERASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN
Itf6 A 239 400 9.6e-36 -0.06 0.75	400 9.6e-36 -0.06	9.66-36 -0.06	-0.06	П	0.75		TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE;	COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX

PDB annotation	(TRANSCRIPTION REGULATIONDNA), RNA POLYMEASE III, 2 TRANSCRIPTION INITIATION, ZINC FINGER PROTEIN			COMPLEX (TRANSCRIPTION REGULATION/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA), RNA REGULATION/DNA), RNA POLYMERAES III, 2 TRANSCRIPTION INTILATION, ZNC FRANSCRIPTION INTILATION, ZNC		The state of the s
Coumpound	CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; SS RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; SS RIBOSOMAL RNA GENB; CHAIN: B, C, E, F;	TFIIIA; CHAIN: A, D; 5S RIBOSOMAL RNA GENE; CHAIN: B, C, E, F;	
SEQFOL D seare		107.85				
PMF			0.99	1.00	0.95	
Verify			-0.02	0.12	0.17	
Psi Blast		7.5e-68	86-38	4.8e-38	8e-34	
END		471	454	511	531	
STAR		310	=======================================	367	395	
CHAI		4	∢	∢	A	
EDB EDB		911	1476	116	1116	
SEQ No ib		1877	1877	1877	1877	1

PDB annotation	RECULATIONDNAY) YING-YANG I; TRANSCRIPTION INITIATION INITIATIOR ELEMENT, YYI, ZINC 2 FINGER FOOTEN, INAL-PROTEIN RECOGNITION, 3 COMPLEX (FRANSCRIPTION, 3 CAMPLEX REGULATIONDA)	COMPLEX (TRANSCRIPTION REGILATION/DIN), TNG-Y-SANG I; TRANSCRIPTION, INITIATION, INITIATION, ELBERT, YYI, ZINC2 FINGER PROTEIN, DIA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DIA)	COMPLEX (TRANSCEPTION REGILATION/DIN) YNG-Y-SANG I; TRANSCRIPTON BUTLATION, INITACOR ELMENT, YY, ZNO.2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCREPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGILATION/DNA) YNG-Y-SANG 1; TRANSCRIPTION, INTLATION, INTLATOR ELBERDI, YYI, ZING 2 PINGER PROTEIN, DNA-PROTEIN RECOGNITION, 20 COMPLEX (TRANSCRIPTION)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG I; TRANSCRIPTION INITIATION,
Coumpound	ASSOCIATED VIRUS PS INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CRAIN; C; ADBNO- SSOCIATED VIRUS PS INITIATOR ELEMENT DIM; CHAIN; A, B;	YYI; CIAIN: C; ADBNO- SASOCIATED VIRUS PS INITIATOR ELEMENT DNA; CHAIN: A, B;	YYI; CIAIN; C; ADBNO- SSOCIATED VIRUS PS INITIATOR ELEMENT DIA; CHAIN; A, B;	YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA;
SEQFOL D score					
PMF		86.0	0.86	00'1	0.95
Verify		-0.00	-0.09	00:00	-0.13
Psi Blast		7.5e-40	6.4e-33	3e-50	3.2e-35
END		363	363	391	419
STAR T AA		243	246	287	318
CHAI N 1D		O	o	၁	С
PDB ID		lubd	1ubd	lubd	Inbd
SEQ No.		1877	1877	1877	1877

PDB annotation	INITIATOR ELEMENT, YYI, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATIONIDNA)	COMPLEX (TRANSCRIPTION REGULATION/UNA) TING-YANG I; TRANSCRIPTION INITIATION, INITIACOR, ELEMENT, YYI, ZINC2 FINGER PROTER, DAM, PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DAY) YING-YANG I; TRANSCRIPTION, INITIATION, INITIATON, EINERNI, YY1, ZINC2 HINGER PROTEIN, DIA,-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRPTION REGULATION/DAY) YING-YANG I; TRANSCRIPTION, INITIATION, INITIATOR ELBERNI, YY1, ZINC2 FINGER PROTEIN, DIA,-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCREPTION)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG I; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTTEN INA PROTEIN
Соитроип	CHAIN: A, B;	YYI; CIIAIN: C; ADENO- ASSOCIATED VIRUS P5 INITATOR ELEMENT DNA; CHAIN: A, B;	YYI; CHANY, C; ADENO- ASSOCIATED VIRUS PS INITIATOR ELEMENT DNA; CHAIN; A, B;	YYI; CBADN: C; ADBNO- ASSOCIATED YIRUS PS INITATOR ELEMENT DNA; CHADN: A, B;	YYI; CHAIN: C; ADENO. ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;
SEQFOL D score		86.32			
PMF			66'0	0.95	0.99
Verify			0.26	0.03	0.10
Psi Blast		3c-48	1.1e-47	4.8e-32	3e-48
END		448	474	473	501
STAR T AA		340	364	374	392
CHAI N ID		ပ	o	Ü	S
PDB ID		lubd	Jubd	1ubd	1ubd
SEQ NO:		1877	1877	1877	1877

PDB annotation	RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1;	TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2	FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX	(TRANSCRIPTION REGULATION/DNA)	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1;	TRANSCRIPTION INITIATION,	INITIATOR ELEMENT, YY1, ZINC 2	RECOGNITION, 3 COMPLEX	(TRANSCRIPTION	REGULATION/DNA)	TRANSCRIPTION REGULATION	TRANSCRIPTION REGULATION,	ADKI, ZINC FINGER, NMR	TE ANSCRIPTION REGULATION	ADRI, ZINC FINGER, NMR	COMPLEX (DNA-BINDING	PROTEIN/DNA) FIVE-FINGER GLI;	GLI, ZINC FINGER, COMPLEX (DNA-	COMPLEX ONA-BINDING	PROTEINDNA) FIVE-FINGER GLI:	GLI, ZINC FINGER, COMPLEX (DNA-	BINDING PROTEIN/DNA)	COMMINION AND VINES
Coumpound		YY1; CHAIN: C; ADENO- ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA; CHAIN: A, B;			YYI; CHAIN: C; ADENO- ASSOCIATED VIRUS P5	INITIATOR ELEMENT DNA;	CHAIN: A, B;				ADRI; CHAIN: NULL;		Appl. Office Num.	ADKI; CHAIN: NOLL;		ZINC FINGER PROTEIN GLII;	CHAIN: A; DNA; CHAIN: C, D;		ZINC FINGER PROTEIN GLII-	CHAIN: A; DNA; CHAIN: C, D;			PINIC EINIGED DEOTERN CT 11.
SEQFOL D score																								93.76
PMF		1.00				1.00						0.41		0.63	0.00		0.80			0.41				
Verify		0.12				-0.08						-0.48		0.00	67.0		0.15			0.19				
Psi Blast		1.5e-48				8e-34						1.3e-14		1 60 10	71-20-1		1.5e-46			3.2e-33				1.50-66
END AA		230				529	_					516		300	200		365			390				421
STAR T AA		450				430						162		220	ŝ		190			246				282
CHAI N ID		၁				U											¥			A				٧
aga gi		pqnı				lubd						2adr		Sock	- I		2gli			2eli				2gli
SEQ No io		1877				1877						1877		1077	7,01		1877			1877		_		1877

	PDB CHAI	M STAR D TAA	END AA	Psi Blast	Verify	PMF	SEQFOL D score	Coumpound	PDB annotation
1		-	_					CHAIN: A; DNA; CHAIN: C, D;	PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)
2gli	∢	310	503	1.5e-66	-0.16	0.27		ZINC FINGER PROTEIN GLII; CFIAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEINIDNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEINIDNA)
2gli	<	395	533	60-53	-0.16	0.93		ZINC FINGER PROTEIN GLII; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA- BINDING PROTEIN/DNA)
1424	4	160	424	3.20c.15		I	65.03	N.ETHVI MAI BIMIDE.	HEX AMEDIZATION DOMAIN
								SENSITIVE FUSION PROTEIN; CHAIN: A:	HEXAMERIZATION DOMAIN, ATPASE, TRANSPORT
1d2n	¥	196	349	3.2e-15	0.35	0.64		N-ETHYLMALEIMIDE- SENSITIVE FUSION PROTEIN; CHAIN: A;	HEXAMERIZATION DOMAIN HEXAMERIZATION DOMAIN, ATPASE, TRANSPORT
1e94	ш	691	270	3.2e-13	-0.74	0.10		HEAT SHOCK PROTEIN HSLV; CHAIN; A, B, C, D; HEAT SHOCK PROTEIN HSLU; CHAIN; E, F;	CHAPERONE HSLV; HSLU CHAPERONE, HSLVU, CLPQY, AAA- ATPASE, ATP-DEPENDENT 2 PROTEOLYSIS, PROTEASOME
lfin	∢	184	405	1.5e-15	0.22	0.28		CELL DIVISION CONTROL PROTEIN 6; CHAIN: A, B;	CELL CYCLE CDG6P; CDC6, CDC18, ORC1, AAA PROTEN, DNA REPLICATION INITATION 2 FACTOR, CELL CYCLE CONTROL FACTOR.
1841	∢	169	360	1.6e-16	0.00	0.57		HEAT SHOCK PROTEIN HSLU; CHAIN: A;	CHAPERONE AAA-ATPASE, CLPY, ATP-DEPENDENT PROTEOLYSIS
lg4I	¥	183	442	4.5e-34	0.16	0.23		HEAT SHOCK PROTEIN HSLU; CHAIN: A;	CHAPERONE AAA-ATPASE, CLPY, ATP-DEPENDENT PROTEOLYSIS
2cmk	⋖	218	245	0.0045	-0.51	0.15		CYTIDINE MONOPHOSPHATE KINASE; CHAIN: A;	TRANSFERASE CK; NUCLEOTIDE MONOPHOSPHATE KINASE, TRANSFERASE

Coumpound PDB annotation	AMINOTRANSFERASE, CHAIN: SANRATATE MANDIOTRANSFERASE, A. B. ILOMD DA-MITTATAR-REPARTE, ILOMD DA-MITTATAR-REPARTE, ILOMD DA-MITTATAR-REPARTE, ILOMD DA-MITATAR-REPARTE, ILOMD D	ASPARTATE AMINOTRANSFERASE CYTOGOLIC ASPARTATE AMINOTRANSFERASE A, B. ILOAND 2-METRYAFPRATTE, ILOAND 2-METRYAFPARTATE, AMINOTRANSFERASE AMINOTRANSFERASE	RRAND ARSHERAKANIN TRANSF RRAND ARSHRAKANI TA E.C.Z.G. I.J. OOMELEXED WITH SASS PYRIDOXAL-5*- PHOSPIATE ARRA FEBONAL-5*- PHOSPIATE ARRA FEBONAL FEBONAL ARRA FEBONAL FEBONAL ARRA FEBONAL ARRA FEBONAL FEBON	RRASD ASPERDASE/AMNOTRANSF RRASD ASPACTATE GR.C.S.G.LI) COMPLEXED WITH GR.C.S.G.LI) COMPLEXED WITH FREE PYRIDOXAL-5: PHOSPIATE AREA	TRYPTOPHANDSE; CHAIN: A. TRYPTOPHAN BIGGYNTHESIS B, C, D, TRYPTOPHAN INOLE-IVASE; TRYPTOPHAN INOLE-IVASE; TRYPTOPHAN INOLE-IVASE; TRYPTOPHAN INOLE-IVASE; PWINDOAL 25 "PHOSPHATE, PWINDOAL 25 "PHOSPHATE, MONOVALENT CATTON BINDING SITTE	1-AMINOCYCLOPROPANE-1- CARBOXYLA IE SYNTHASE; ADENOSYL-L-METHONINB CARBOXYLA IE SYNTHASE; ADENOSYLA IE SYNTHASE IE SYNTHASE; ADENOSYLA IE
	ASPARTATE AMINOTRANS A, B;	ASPARTATE AMINOTRANS A, B;	TRANSFERASE(AMING ERASE) ASPARTATE AMINOTRANSFERASE (E.C.2.6.1.1) COMPLEXI 1ARS 3 PYRIDOXAL-5-1 PHOSPHATE IARS 4	TRANSFERASE(AMING ERASE) ASPARTATE AMINOTRANSEERASE (E.C.2.6.1.1) COMPLEXI IARS 3 PYRIDOXAL-5: PHOSPHATE IARS 4	TRYPTOPHAN B, C, D;	L-AMINOCYCI CARBOXYLA' CHAIN: A B:
IF SEQFOL	77.13			76.94	71.45	
PMF		0.88	0.51			00:1
Verify		0.08	-0.19			0.44
Psi Blast	1.6e-58	1.6e-58	1.6e-64	1.6e-64	4.8e-13	0
END	499	517	457	208	523	515
STAR T AA	25	\$	82	56	89	08
CHAI N ID	4	₹.			₹.	∢
PDB ID	lajs	Iajs	Iars	lars	Iax4	168g
SEQ NO:	1882	1882	1882	1882	1882	1882

		Ä	j.			1				
PDB annotation	GENE) AHBA SYNTHASE; RIFAMYCIN BIOSYNTHESIS (RIFD GENE)	AMINOTRANSFERASE AMINOTRANSFERASE, PYRIDOXAL ENZYME	AMINOTRANSFERASE AMINOTRANSFERASE, PYRIDOXAL ENZYME	TRANSFERASE TAT; TYROSINE CATABOLISM, TRANSFERASE, AMINOTRANSFERASE, 2 PYRIDOXAL-S:-PHOSPHATE, PLP	TRANSFERASE TAT; TYROSINE CATABOLISM, TRANSFERASE, AMINOTRANSFERASE, 2 PYRIDOXAL-5'-PHOSPHATE, PLP	TRANSFERASE TRANSFERASE, AMINOTRANSFERASE, PYRIDOXAL PHOSPHATE	LYASE CGS; LYASE, LLP- DEPENDENT ENZYMES, METHIONINE BIOSYNTHESIS	TRANSFERASE AMINOTRANSFERASE FOLD, LARGE PLP-BINDING DOMAIN, SMALL C-2 TERMINAL DOWAIN, OPEN ALPHA-BETA STRUCTURE.	TRANSFERASE SHMT, SERINE METHYLASE; ALPHA PLP ASPARTATE, AMINO TRANSFERASE, (AAT)-LIKE FOLD	LYASE FES CLUSTER BIOSYNTHESIS, PYRIDOXAL 5'-
Coumpound	HYDROXYBENZOIC ACID SYNTHASB; CHAIN: A;	ASPARTATE AMINOTRANSFERASE; CHAIN: A, B;	ASPARTATE AMINOTRANSFERASE; CHAIN: A, B;	TYROSINE AMINOTRANSFERASE; CHAIN: A, B;	TYROSINE AMINOTRANSFERASE; CHAIN: A, B;	CYSTALYSIN; CHAIN: A, B, C, D, E, F, G, H;	CYSTATHIONINE GAMMA- SYNTHASE; CHAIN: A, B, C, D;	MALY PROTBIN; CHAIN: A, B;	SERINE HYDROXYMETHYLTRANSFER ASE; CHAIN: A, B, C, D;	L-CYSTEINE/L-CYSTINE C-S LYASE; CHAIN: A, B;
SEQFOL D score			134.98		158.29					
PMF		1.00		1.00		1.00	0.13	00:1	00:1	0.87
Verify score		0.52		0.24		0.34	-0.10	0.35	0.42	0.17
Psi Blast		9.6e-84	9.6e-84	1.6e-67	1.6e-67	6e-52	1.6e-08	4.5e-53	4.8e-07	9.6e-13
END		515	514	520	520	514	302	514	415	514
STAR T AA		102	83	99	35	125	144	128	182	123
CHAI N ID		<	A	A	V	∀	A	¥	∢	A
PDB ID		1bjw	1bjw	1bw0	1bw0	lc7n	lcs1	ld2f	idfo	lelu
SEQ ID NO:		1882	1882	1882	1882	1882	1882	1882	1882	1882

und PDB annotation	PHOSPHATE, 2 THIOCYSTEINE, AMINOACRYLATE, ENZYME- PRODUCT COMPLEX	AMINOTRANSFERASE TRANSFERASE, AMINOTRANSFERASE	AMINOTRANSFERASE TRANSFERASE, AMINOTRANSFERASE	HAIN:	O ACID AMINOTRANSFERASE AROAT; ASE; CHAIN: AMINOTRANSFERASE	MINOTRANSF TF AASB AASB H H SSPHTE SST 4	MINOTRANSE TE AASE LIJ 2CST 3 H H SOSPHATE ST 4	DL-LYASE; LYASE LYASE, PLP-DEPENDENT ENZYME, PYRIDOXAL PHOSPHATE	-
Coumpound		ASPARTATE AMINOTRANSFERASE; CHAIN: A. B. C. D:	ASPARTATE AMINOTRANSFERASE; CHAIN: A. B. C. D:	AROMATIC AMINO ACID AMINOTRANSFERASE; CHAIN: A, B;	AROMATIC AMINO ACID AMINOTRANSFERASE; CHAIN: A. B:	TRANSFERASE(AMINOTRANSF BRAASI) ASPARTATE AMINOTRANSFERASE (CASPAT) (E.C.2.6.1.1) 2CST 3 COMPLEXED WITH PYRIDOXAL-5-PHOSPHATE AND MALEATE 2CST 4	TRANSFERA SE(AMINOTRANSF BRASE) ASPATIATE AMINOTRANSFERASE (CASPAT) (E.C.2.6.1.1) 2CST 3 (COMPLEXED WITH PYRIDOXAL-S-PHOSPHATE AND MALEATE 2CST 4	TYROSINE PHENOL-LYASE; CHAIN: A, B;	TYROSINE AMERICA CHARL
SEQFOL D score		79.51		74.67			75.00		
PMF			0.1		0.88	0.95		0.34	0.95
Verify score			90.06		-0.16	-0.13		10.0	-0.17
Psi Blast		4.8e-52	4.8e-52	8e-53	8e-53	1.6e-58	1.6e-58	1.1e-48	9.6e-58
END		516	452	488	457	517	499	208	457
STAR		92	68	79	88	81	88	011	08
CHAI		∢	¥	V	A	⋖	∢	<	A
EDB CI		lyaa	lyaa	2ay1	2ayl	2cst	2cst	2tp1	3tat
S e S		1882	1882	1882	1882	1882	1882	1882	1882

PDB annotation	SUBSTRATES, PLP ENZYME	AMINOTRANSFERASE PHEAT, TYRAT, AROAT;	AMINOTRANSFERASE, AROMATIC SUBSTRATES, PLP ENZYME									HYDROLASE TYROSINE PHOSPHATFASE 1 AR PROTEIN	HYDROLASE DIJAL SPECIFICITY	PHOSPHATASE, MAP KINASE	HVDPOI ASE DITAL SECTEDITIV	PHOSPHATASE, MAP KINASE HYDROLASE	HYDROLASE VHR; HYDROLASE,	PROTEIN DUAL-SPECIFICITY PHOSPHATASE	HYDROLASE VHR; HYDROLASE,	PROTEIN DUAL-SPECIFICITY PHOSPHATASE	IMMUNOGLOBULIN
Coumpound		TYROSINE AMINOTRANSFERASE; CHAIN:	A, B, C, D, E, F;	TRANSFERASE(AMINOTRANSF	ERASE) ASPARTATE AMINOTRANSFERASE	(E.C.2.6.1.1) COMPLEX WITH	PHOSPHATE AT PH 7.5 7AAT 4	TRANSFERASE(AMINOTRANSF ERASE) ASPARTATE	AMINOTRANSFERASE	(E.C.2.6.1.1) COMPLEX WITH 7AAT 3 PYRIDOXAL-5'-	PHOSPHATE AT PH 7.5 7AAT 4	LAR; CHAIN: A, B;	PYSTI: CHAIN: NIJI I.:		DVCT1. CUAIN: NIII I .	risti, chain: NOLE,	HUMAN VHI-RELATED DUAL-	SPECIFICITY PHOSPHATASE CHAIN: A. B;	HUMAN VHI-RELATED DUAL-	SPECIFICITY PHOSPHATASE	ANTIBODY CTM01; CHAIN: L,
SEQFOL D score		91.42						78.03					68.80				139.04				
PMF				0.43								81.0			1 00	3			1.00		I.00
Verify				-0.10								-0.13			0.57				0.74		0.30
Psi Blast		9.6e-58		6.4e-65				6.4e-65				1.1c-58	6.4e-24		bC-049	17000	7.5e-31		7.5e-31		9.6e-82
END AA		497		457				492				220	200		200	204	208		200		242
STAR		56		73				88				6	52		35	3	37		50		20
CHAI N ID		A		A				A				ш					A		A		н
PDB		3tat		7aat				7aat				llar	Imko		Imkn		lvhr		lvhr		lae6
SEQ NO:		1882		1882				1882				1883	1883		1883	}	1883		1883		1884

SEQ NO:	PDB ID	CHAI N ID	STAR T AA	END	Psi Blast	Verify score	PMF	SEQFOL D score	Coumpound	PDB annotation
									£	IMMUNOGLOBULIN, FAB FRAGMENT, HUMANISATION
1884	lafv	н	20	244	86-84	0.43	1.00		HUMAN IMMUNODERICIENCY VIREN TYPE I CARSID CHAIN: A. B. ANTIBODY FAB25.3 FRAGMENT; CHAIN: H, K, L, M;	COMPLEX (VIRAL CARIDIAMUNOCOLBULIA) HIV-I CA, HIV CA, HIV P24, P24; FAB, FAB LIGHT CHAIN, FAB HEA VY CHAIN COMPLEX (VIRAL) CAPSIDIMAUNOCOLBULIA), HIV, CAPSIDIMAUNOCOLBULIA), HIV,
1884	1Pd2	បា	21	261	1.2e-81			301.81	HIA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN: G; TAX PETIDE; CHAIN: G; CELL RECEPTOR, ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: G;	COMPLEX (MHC/VIRAL PEPTIDEACESPTOR) HEAVY CHAIN; COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)
1884	1bd2	ъ	22	261	1.2e-81	0.66	1.00		HLA-A (201; CHAIN: A; BETA-2 MCROGLOBULIN: CHAIN: B; TAX PETTIDE, CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA: CHAIN: E	COMPLEX (MHC/VIRAL PBTIDE/REGEPTON, HIA A2 HEA YY CHAIN; COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)
1884	Ibec		21	261	1.5e-76			273.44	14.3.D T CELL ANTIGEN RECEPTOR; IBEC 5 CHAIN: NULL; IBEC 6	RECEPTOR T CELL RECEPTOR 1BEC 14
1884	1451	Н	20	244	1.3e-81	0.23	66'0		CHIMERIC GERMLINE PRECIRSOR OF OXY-COPE CHAIN: L; CHIMERIC GERMLINE PRECURSOR OF OXY-COPE CHAIN: H;	IMMUNE SYSTEM IMMUNE SYSTEM
1884	le60	H	20	244	4.8e-81	0.40	1.00		IMMUNOGLOBULIN LIGHT CHAIN; CHAIN: L; IMMUNOGLOBULIN HEAVY CHAIN; CHAIN: H:	IMMUNOGLOBULIN FAB, ANTIBODY, ANTIGEN, HIV-1, P24, CA
1884	J-J-J	В	20	247	1.1c-84	0.18	1.00		IMMUNOGLOBULIN FAB	

PDB annotation			IMMUNOGLOBULIN INTACT	IMMUNOGLOBULIN V REGION C REGION, IMMUNOGLOBULIN	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN, V REGION, C	IMMUNOGLOBULIN	IMMÜNÖGLÖBÜLIN VARİABLE HEAYY (YIV) DOMANI, VARİABLE LIGHT (YL), ANTIBODY FRAGMENT, MULTIVALENT ANTIBODY, DARDÜY, DOMANIN 2 SWAPPING, DAMANINGT CORITIN	RECEPTOR TCR. T-CELL, RECEPTOR, TRANSMEMBRANE, GLYCOPROTEIN, SIGNAL	CHAPERONE AAA-ATPASE, CLPY, ATP-DEPENDENT PROTEOLYSIS	GENE REGULATION POZ DOMAIN; PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCRIPTIONAL 2
Coumpound	FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 IFVD 3	COMPLEX (ANTIBODY/BINDING PROTEIN) IGGI FAB FRAGMENT COMPLEXED WITH PROTEIN G (DOMAIN III) 11GC S PROTEIN G,	STREPTOCOCCUS 11GC 15 IGG2A INTACT ANTIBODY -	MAB231; CHAIN: A, B, C, D	IGGI INTACT ANTIBODY MAB61.1.3; CHAIN: A, B, C, D	NIG9 (IGGI=LAMBDA=); CHAIN; L. H;	SINGLE-CHAIN ANTIBODY FRAGMENT; CHAIN: A, C;	ALPHA, BETA T-CELL RECEPTOR CHAIN: A, B;	HEAT SHOCK PROTEIN HSLU; CHAIN: A;	PROMYBLOCYTIC LEUKEMIA ZINC FINGER PROTEIN PLZF; CHAIN; A;
SEQFOL D score								277.99		
PMF		1.00	96:0		0.82	1.00	1.00		0.04	1.00
Verify		0.22	-0.00		0.07	0.21	0.22		-0.34	0.34
Psi Blast		1.6c-83	3.2e-90		3.2e-82	1.6e-83	9c-07	8e-71	0.0094	4.8e-24
END		247	282		282	244	130	262	369	129
STAR T AA		20	20		21	20	12	19	314	9
CHAI N ID		Ħ	В		æ	Ξ	<	В	V	<
PDB ID		ogi1	ligt		ligy	Ingp	Ingb	Iter	1g41	onqI
SEQ ID NO:		1884	1884		1884	1884	1884	1884	1885	1886

					\neg		r	
PDB annotation	REPRESSOR, ZINC-FINGER PROTEIN, X-RAY CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION	GENE REGILATION POZ DOMANN, PROTEIN-PROTEIN INTERACTION DOMAIN, TRANSCREPTIONAL 2 REPRESSOR, ZINC-FINGER PROTEIN, X-RAY CRYSTALLOGRAPHY, 3 PROTEIN STRUCTURE, PROMYELOCYTIC LEUKEMIA, GENE REGULATION				RNA-BINDING PROTEINRNA TRA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPI FX	GENE REGULATION/RNA POLY(A) BYDING PROTEN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
Coumpound		PROMYELOCYTIC LEGGEMIA ZINC FINGER PROTEIN PLZF; CHAIN: A;	OXIDOREDUCTASE(OXYGEN(A)) GALACTOSE OXIDASE (E.C.1.1.3.9) (PH 4.5) 1GOF 3	OXIDOREDUCTASE(OXYGEN(A)) GALACTOSE OXIDASE (E.C.1.1.3.9) (PH 4.5) 1G0F 3		SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'- R(P*GP*UP*UP*UP*UP*UP* UP*UP*IP*IP*IP*IP*IP*IP*	POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA, (5- R(*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*A	POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (5'- R(*AP*AP*AP*AP*AP*AP*AP*
SEQFOL D score		59.44						
PMF			0.27	0.12		0.1	1.00	0.89
Verify score			0.31	0.36		0.53	0.41	0.41
Psi Blast		4.8e-24	1.2e-32	6.4e-12		9e-03	3c-05	30-05
END AA		134	551	555		1410	1410	1410
STAR T AA		6	291	301		1342	1342	1340
CHAI N ID		¥				<	<	g
PDB ID		1buo	1gof	1gof		1671	leyj	lovj
SEQ NO:		1886	1886	1886	2000	1887	1887	1887

PDB annotation		RNA BINDING PROTEIN RNA- BINDING DOMAIN	STRUCTURAL PROTEIN PROTEIN C23; RNP, RBD, RRM, RNA BINDING DOMAIN, NUCLEOLUS	OUTER MEMBRANE PROTEIN OSMOPORIN; OUTER MEMBRANE PROTEIN, NON-SPECIFIC PORIN, OSMOPORIN, 2 BETA-BARREL,	TRANSMEMBRANE	HYDROLASE DOUBLE BETA BARREL, BACTERIAL SERINE PROTEASE		RNA-BINDING DOMAIN RNA- BINDING DOMAIN, ALTERNATIVE SPLICING	RNA-BINDING PROTEIN SPLICING, U2 SNRNP, RBD, RNA-BINDING PROTEIN	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2
Coumpound	AP*AP*AP*A); CHAIN: M, N, O, P, Q, R, S, T;	HU ANTIGEN C; CHAIN: A;	NUCLEOLIN RBD2; CHAIN: A;	OMPK36; CHAIN: A, B, C;	OUTER MEMBRANE PROTEIN PHOSPHOPORIN (PHOE) 1 PHO 3	ALPHA-LYTIC PROTEASE; CHAIN: A;	RNA-BINDING PROTEIN SEX- FEHAL PROTEIN (C. TERMINUS, OR SECOND RIA- BINDING DOMAIN 1SXL 3 (RBD-2), RESIDUES 199-294 PLUS N-TERMINAL MET) 1SXL 4 (NMR, 17 STRUCTURES) 1SXL	SEX-LETHAL PROTEIN; CHAIN: NULL;	SPLICING FACTOR UZAF 65 KD SUBUNIT; CHAIN: A;	SEX-LETHAL; CHAIN: A, B, C;
SEQFOL D score										
PMF		00'1	0.65	-0.20	-0.19	-0.19	0.54	1.00	0.99	0.55
Verify		0.45	0.42	0.70	0.77	0.89	0.07	0.47	0.44	0.01
Psi Blast		4.5e-05	3e-05	4.5e-09	7.5e-10	4.5e-08	0.00015	0.00015	1.3e-05	6e-05
END		1410	1417	207	218	204	1396	1410	1410	1432
STAR T AA		1342	1331	14	=	37	1325	1339	1342	1339
CHAI N ID		A	¥	∢		4			<	4
PDB ID		148z	og 1	losm	Ipho	Iqq4	lsxl	2sxl	2u2f	3sxl
SEQ NO:		1887	1887	1887	1887	1887	1887	1887	1887	1887

1303 1371 59-05 0.53 1.00 SXL-LETHAL PROTEIN; CHAIN; R. A. B. RAM, C. B. RAM, C. B. RAM, C. B. RAM, C. B. RAM, C. B. RAM, C. B. RAM, C. B. RAM, C. B. RAM, C. B. C. D. E. G. B. R. G. D. E. G. B. R. RAM, C. B. C. D. E. G. B. R. RAM, C. B. C. D. E. G. D. R. R. P. C. D. E. G. D. R. R. P. C. D. E. G. D. R. R. P. C. D. E. G. D. R. R. P. C. D. E. G. D. C. D. E. G. D. C. D. C. B. C. D. C.	PDB C	CHAI N ID	I STAR T AA	END	Psi Blast	Verify	PMF	SEQFOL D score	Coumpound	PDB annotation
1371 96-65 0.53 1.00 SXL-LETHALPROTEBIÇ GHANN. A B. RNA C. A B. RNA C. A B. RNA C. A B. RNA C. B. RNA C. B. RNA C. B. RNA C. B. RNA C. B. RNA C. B. RNA C. B. RNA C. B. RNA C. B. R. C. D. B. C. B. E. G. B. R. RNA C. B. C. D. B. C. B. E. G. B. R. RNA C. B. R. RNA C. B. R. RNA C. B. R. RNA C. B. E. G. B. R. RNA C. B. C. D. B. C. B. E. G. B. RNA C. B. RNA C. B. C. D. E. C. B. E. G. B. RNA C. B. C. D. E. C. B. E. G. B. RNA C. B. C. D. E. C. B. E. G. B. RNA C. B. C. D. E. G. B. RNA C. B. C. D. E. G. B. C. B. C. D. E. C. B. C. B. C. D. E. C. B. C. B. C. D. B. C. D. E. C. B. C. B. C. D. B. C. D. E. C. B. C. D. B. C. D. E. C										SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION
1371 36-05 0.41 1.00 POLYDEWLAP OF UP-UP-UP-UP-UP-UP-UP-UP-UP-UP-UP-UP-UP-U	1b7f A		1303	1371	9e-05	0.53	1.00		PROTEIN; CHAIN:	
1371 3-645 0.44 1.00			_						A, B; RNA (5'-	PRE-MRNA; SPLICING
1371 36-65 641 1.00 PROTIDENTALE BINDING TO PROTINELY I, CIANIN A. B. C. D. E. G. HENG, (S. A. L. C. D. E. G. HENG, (S. A. L. C. D. E. G. HENG, (S. A. L. C. D. E. G. HENG, (S. A. L. C. D. E. G. HENG, (S. A. L. C. D. E. G. HENG, (S. A. L. C. D. E. G. HENG, (S. A. L. C. D. E. G. HENG, (S. A. L. C. D. E. G. HENG, (S. A. L. C. D. E. G. HENG, (S. A. L. C. D. E. G. HENG, (S. A. L. C. D. E. G. HENG, (S. A. L. C. D. E. G. HENG, (S. A. L. C. D. E. G. HENG, (S. A. L. C. D. E. G. HENG, (S. A. L. G. D. E. G. HENG, (S. A. L. G. D. E. G. HENG, (S. A. L. G. D. E. G. HENG, (S. A. L. G. D. E. G. HENG, (S. A. L. G. D. E. G. HENG, (S. A. L. G. D. E. G. HENG, (S. A. L. G. D. E. G. HENG, (S. A. L. G. D. L. G. HENG, (S. A. L. G. D. L. G. HENG, (S. A. L. G. D. L. G. HENG, (S. A. L. G. D. L. G. HENG, (S. A. L. G. D. L. G. HENG, (S. G. HENG, G. G. HENG, G. G. HENG, (S. A. L. G. D. L. G. HENG, (G. G. HENG, G. G. HENG, (G. HENG, G. HENG, G. G. HENG, (G. HENG, G. HENG, G. HENG, (G. HENG, G. HENG, G. HENG, G. HENG, (G. HENG, G. HENG, G. HENG, G. HENG, (G. HENG, G. HENG, G. HENG, G. HENG, G. HENG, G. HENG, (G. HENG, G. HE	_								UP*UP*UP*UP*U)- CHAIN: P, Q;	KEGULA HUN, KNP DOMAIN, KNA COMPLEX
ROTENIA (GARNA A.B. C. D. B. F. G. H. RNA (G. TRAINA A.B. C. D. B. F. G. H. RNA (G. TRAINA A.B. C. D. B. F. G. H. RNA (G. TRAINA A.B. C. D. F. G. H. RNA (G. TRAINA A.B. C. D. P. Q. R.S.) TO GARNA A.B. C. D. E. G. G. H. RNA (G. TRAINA A.B. C. D. E. F. G. H. RNA (G. TRAINA A.B. C. D. E. F. G. H. RNA (G. TRAINA A.B. C. D. E. F. G. H. RNA (G. TRAINA A.B. C. D. E. F. G. H. RNA (G. TRAINA A.B. C. D. C. D. G. G. G. G. G. G. G. G. G. G. G. G. G.	lcvj A		1303	1371	3e-05	0.41	1.00		POLYDENYLATE BINDING	GENE REGULATION/RNA POLY(A)
F. G. IR. MA. APA-PRA-PRA-PRA-PRA-PRA-PRA-PRA-PRA-PRA-									PROTEIN I; CHAIN: A, B, C, D,	BINDING PROTEIN 1, PABP 1; RRM,
									E, F, G, H; RNA (5'-	PROTEIN-RNA COMPLEX, GENE
1301 1371 36-05 0.41 0.89 POLYDENTYLTEBINDING POLYDENTYLTBINDING POLYDENTYLTBINDING POLYDENT	_								R(*AP*AP*AP*AP*AP*AP*	REGULATION/RNA
130 137 36-65 0.41 0.89 POLYDENYATE BIONDO PROTEIN I; CHARK ALE BIONDO PROTEIN I; CHARK ALE BIONDO PROTEIN I; CHARK ALE BIONDO PROTEIN I; CHARK ALE ALE ALE ALE ALE ALE ALE ALE ALE ALE									O. P. O. R. S. T.	
RWOTENI LEGHAN A, B, D, B, E, D, H, RAM, G [*] . RWOTENI LEGHAN, A, B, D, B, E, D, H, RAM, G [*] . RWOTENI LEGHAN, A, B, D, B, E, D, H, RAM, G [*] . RWOTENI LEGHAN, A, B, D, D, D, B, E, D, H, RAM, G [*] . RWOTENI LEGHAN, A, B, D, D, D, E, E, D, E, E, D, E, E, D, E, E, D, E, E, D, E, E, D, E, E, D, E, E, D, E, E, D, E, E, D, E, E, D, E, E, E, D, E, E, E, E, E, E, E, E, E, E, E, E, E,	lcvj B		1301	1371	3e-05	0.41	0.89		POLYDENYLATE BINDING	GENE REGULATION/RNA POLY(A)
1303 1371 4.5e-05 0.45 1.00 1.0 F, C, H, RAPAPA, APPAPA, A									PROTEIN I; CHAIN: A, B, C, D,	BINDING PROTEIN 1, PABP 1; RRM,
1303 1371 4.5e-d5 0.45 1.00			_						E, F, G, H; RNA (5'-	PROTEIN-RNA COMPLEX, GENE
1303 1371 4.5e-05 0.45 1.00 1.0 P. 0.8, S. T. 1202 1378 3e-05 0.42 0.65 1.00 1.0 ANTGEN C; CHAIN: A; 14 207 4.5e-09 0.70 -0.20 0.0/IVEB MEMBRANE PROTEIN 1 218 7.5e-10 0.77 -0.19 0.0/IVEB MEMBRANE PROTEIN 37 204 4.5e-08 0.39 -0.19 ALPHA-LYTIC PROTEIN	_								R(*AP*AP*AP*AP*AP*AP*	REGULATION/RNA
1303 1371 4.5e-05 0.45 1.00 HUANTGEN C; CHAIN: A; 1202 1378 3e-05 0.42 0.65 NUCLEOLIN RBD2; CHAIN: A; 14 207 4.5e-09 0.70 -0.20 OMPK36; CHAIN: A, B, C; 11 218 7.5e-10 0.77 -0.19 OUTER MEMBRANE PROTEIN 11 218 7.5e-10 0.77 -0.19 OUTER MEMBRANE PROTEIN 137 204 4.5e-08 0.89 -0.19 ALPHA-LYTIC PROTEIN (PHOLIPHOSTE).	_								AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	
1292 1378 36-05 0.42 0.65 NUCLEOLIN RBD2; CHAIN: A; 14 207 4.56-09 0.70 -0.20 OMPK36; CIJAIN: A, B, C;	Id8z A		1303	1371	4.5e-05	0.45	1.00		HU ANTIGEN C; CHAIN: A;	RNA BINDING PROTEIN RNA- BINDING DOMAIN
14 207 4.5e-69 0.70 -0.20 OMPKJG; CHAIN: A. B. C;	Ifje A		1292	1378	3e-05	0.42	0.65		NUCLEOLIN RBD2; CHAIN: A;	STRUCTURAL PROTEIN PROTEIN C23; RNP, RBD, RRM, RNA BINDING
11 218 7.5e-10 0.77 -0.19 OUTER MEMBRANE PROTEIN PROSTHOROW (RHOBE) IPHO 3 37 204 4.5e-08 0.89 -0.19 ALPHA-YTC PROTEINSE.	Iosm A	١.	41	207	4.5e-09	0.70	-0.20		OMPK36; CHAIN: A. B. C.	OUTER MEMBRANE PROTEIN
11 218 7.5e-10 0.77 -0.19 OUTER MEMBRANE PROTEIN PROSPHORON (RPED) PRO 171.0										OSMOPORIN; OUTER MEMBRANE PROTEIN, NON-SPECIFIC PORIN,
11 218 7.5e-10 0.77 -0.19 OUTER MENBRANE PROTEIN PHOSPHOPORIN (PHOE) 1PHO 3 254 4.5e-68 0.89 -0.19 ALPHAL-YTIC PROTEASE.										OSMOPORIN, 2 BETA-BARREL, TRANSMEMBRANE
37 204 4.5e-08 0.89 -0.19 ALPHA-LYTIC PROTEASE;	lpho		=	218	7.5e-10	0.77	-0.19		OUTER MEMBRANE PROTEIN PHOSPHOPORIN (PHOE) 1PHO 3	
	1qq4 A		37	204	П	68.0	-0.19		ALPHA-LYTIC PROTEASE;	HYDROLASE DOUBLE BETA

PDB annotation	BARREL, BACTERIAL SERINE PROTEASE		RNA-BINDING DOMAIN RNA- BINDING DOMAIN, ALTERNATIVE SPLICING	RNA-BINDING PROTEIN SPLICING, U2 SNRNP, RBD, RNA-BINDING PROTEIN	RNA BINDING DOMANIE REA BINDING DOMANIE RBD, RNA RECOGNITION MOTH, RRM, 2 SPLICNG NHEHTON, TRANSLATIONAL INHIBITOS, SEX3 DETERMINATION, CHROMOSOME DOSAGE COMPENSATION	SXL-LETHAL PROTEIN; CHAIN: RNA-BINDING PROTEINRNA TRA A.B. RNA (5'- RQP-QP-QP-QP-QP-QP-QP- REGULATION; RNP DOMAIN; RNA UP-UP-UP-CHAIN: P. O. COMPLEX	GENE REGULATIONRNA POLY(A) BINDING PROTEIN 1, PABF 1; RRM, PROTEIN-RANA COMPLEX, GENE REGULATIONRNA
Coumpound	CHAIN: A;	RNA-BINDING PROTEIN SEX- LETHAL PROTEIN (C TERMINIS, OR SECOND RNA- BINDING DOMENT I SEX. 3 (RBD-2), RESIDIES 199-294 PLUS N-TERMINAL MET) I SXL 4 (NMR, 17 STRUCTURES) I SXL	SEX-LETHAL PROTEIN; CHAIN: RNA-BINDING DOMAIN, ALTERNA-BINDING DOMAIN, ALTERNA-SPLICING	SPLICING FACTOR UZAF 65 KD SUBUNIT; CHAIN: A;	SEX-LETHAL; CHAIN: A, B, C;	SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'- R(P*GP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP*UP	POLYDENYLATE BINDING PROTEIN I; CHAIN: A, B, C, D, E, F, G, H; RNA (3- R(*AP*AP*AP*AP*AP*AP*AP* AP*AP*AP*AP*AP; J); CHAIN: M, N, AP*AP*AP*AP*AP*
SEQFOL D score							
PMF		0.54	1.00	0.99	0.55	9.1	9.1
Verify score		0.07	0.47	0.44	0.01	0.53	0.41
Psi Blast		0.00015	0.00015	1.3e-05	6e-05	9e-05	3e-05
END		1357	1371	1371	1393	1313	1313
STAR T AA		1286	1300	1303	1300	1245	1245
CHAI N ID				٧	<	Ą	٧
PDB		1sxl	2sxl	2u2f	3sxl	167£	levj
SEQ NO:		1888	1888	1888	1888	6881	1889

		_			_				
PDB annotation	GENE REGULATIONRN, POLY(A) BINDING PROTEIN, I, PABP I, RRM, PROTEIN-RNA COMPLEX, GENE REGULATIONRNA	RNA BINDING PROTEIN RNA- BINDING DOMAIN	STRUCTURAL PROTEIN PROTEIN C23; RNP, RBD, RRM, RNA BINDING DOMAIN, NUCLEOLUS	OUTER MEMBRANE PROTEIN OSMOPORIN; OUTER MEMBRANE PROTEIN, NON-SPECIFIC PORIN, OSMOPORIN, 2 BETA-BARREL, TRANSMEMBRANE		HYDROLASE DOUBLE BETA BARREL, BACTERIAL SERINE PROTEASE		RNA-BINDING DOMAIN RNA- BINDING DOMAIN, ALTERNATIVE SPLICING	RNA-BINDING PROTEIN SPLICING, U2 SNRNP, RBD, RNA-BINDING
Coumpound	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA G;* R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*	HU ANTIGEN C; CHAIN: A;	NUCLEOLIN RBD2; CHAIN: A;	OMPK36, CHAIN: A, B, C,	OUTER MEMBRANE PROTEIN PHOSPHOPORIN (PHOE) 1PHO 3	ALPHA-LYTIC PROTEASE; CHAIN: A;	RNA-BINDING PROTEIN SEX. LETHAL PROTEIN (C. TERMINUS, GR SECOND RNA- BINDING DOMANI 15XL 3 (RBD-2), RESIDIES 195-294 PLUS N-TERMINAL MET) 15XL 4 (NMR, 17 STRUCTURES) 15XL 5	SEX-LETHAL PROTEIN; CHAIN: NULL;	SPLICING FACTOR UZAF 65 KD SUBUNIT; CHAIN: A;
SEQFOL D score									
PMF	0.89	1.00	9.65	-0.20	-0.19	61.0-	0.54	1.00	0.99
Verify	0.41	0.45	0.42	0.70	0.77	0.89	0.07	0.47	0.44
Psi Blast	3e-05	4.5e-05	3e-05	4.5e-09	7.5e-10	4.5e-08	0.00015	0.00015	1.3e-05
END	1313	1313	1320	207	218	204	1299	1313	1313
STAR T AA	1243	1245	1234	14	11	37	1228	1242	1245
CHAI N ID	В	A	A	¥		¥			A
FDB TD	Icvj	1d8z	1Üc	Iosm	1pho	1qq4	lsxl	2sxl	2u2f
SEQ No.	1889	1889	6881	1889	1889	1889	1889	1889	1889

	Г	l_,				Т			_			Г				П
PDB annotation	PROTEIN	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-11, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-II, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-II, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN			RNA BINDING PROTEIN/RNA XLRBPA: PROTEIN-RNA COMPLEX	DOUBLE STRANDED RNA,	PROTEIN-RNA 2 INTERACTIONS,	KNA-BINING PROTEIN, KNA BINDING PROTEIN/RNA	SH3 PROTOTYPE WWPROTOTYPE, PROTEIN DESIGN	CELL CYCLE/RNA DSRBDIII; NMR	STRUCTURE, PROTEIN/RNA,	PROTEIN DSRBD, DROSOPHILA,	RNA 2 HAIRPIN	ISOMERASE PINI; PEPTIDYL-
Coumpound		TENASCIN; CHAIN: A, B;	TENASCIN; CHAIN: A, B;	TENASCIN; CHAIN: A, B;	GLYCOPROTEIN FIBRONECTIN (TENTH TYPE III MODULE) (NMR, 36 STRUCTURES) 1TTF 3		DOUBLE STRANDED RNA BINDING PROTEIN A: CHAIN:	A, B; RNA (5'-	R(*GP*GP*CP*GP*CP*G	r"Cr"C)-3'); CHAIN: C, D, E, G;	WWPROTOTYPE; CHAIN: A;	MATERNAL EFFECT PROTEIN	(STAUFEN); CHAIN: A;	STAUFEN DOUBLE-STRANDED	RNA BINDING DOMAIN; CHAIN; B:	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE PINI; PEPTIDYL-
SEQFOL D score																
PMF		0.29	0.12	-0.20	0.49		0.42				0.41	0.70				0.29
Verify score		-0.24	0.09	0.03	0.15		0.30				-0.10	0.57				-0.46
Psi Blast		4.5e-13	9.6e-15	4.8e-15	3e-13		1.1e-07				0.0003	6e-12				90000
END		261	349	450	265		293				49	293				46
STAR		164	169	271	164		230				20	226				=
CHAI		٧	V	A			V.				Ą	¥		-		В
PDB ID		lqr4	lqr4	Iqr4	JH.	0.1.	1dr2				1e0m	lekz				1f8a
SEQ ID NO:		1894	1894	1894	1894		1895				1895	1895				1895

PDB annotation	PROLINE ISOMERASE, WW DOMAIN, PHOSPHOSERINE BINDING	DOUBLE STRANDED RNA BINDING DOMAIN STAUFEN 1STU 13	
Coumpound	ISOMERASE NIMA- CHAIN; B; Y(SEP)PT(SEP)S PEPTIDE; CHAIN; C;	MATERNAL EFFECT PROTEIN STAUFEN; ISTU 4	
PMF SEQFOL score			
PMF		0.25	
Verify score		0.18	
SEQ PDB CHAI STAR END Psi Blast Verify ID ID NID TAA AA score NO: NO: NO: NO: NO: NO:		3e-05	
END		293 3e-05	
STAR		233	
CHAI			
PDB ID		lstu	
SEQ ID NO:		1895 1stu	

TABLE 6

SEQ ID NO:	Position of Signal in Amino Acid SEquence	maxS (Maximum score)	meanS (Mean score)
949	24	0.926	0.738
950	24	0.976	0.913
951	22	0.982	0.872
952	41	0.937	0.604
953	23	0.896	0.747
954	16	0.945	0.737
955	45	0.964	0.657
956	48	0.994	0.855
957	31	0.984	0.921
958	23	0.966	0.812
959	36	0.994	0.757
960	20	0.977	0.902
961	18	0.968	0.799
962	24	0.882	0.599
963	34	0.921	0.652
964	25	0.921	0.787
965	33	0.967	0.803
966	30	0.978	0.786
967	28	0.980	0.893
968	24	0.976	0.913
969	22	0.984	0.928
970	26	0.949	0.664
971	23	0.996	0.936
972	28	0.929	0.700
973	26	0.976	0.875
974	17	0.919	0.828
975	28	0.976	0.653
976	30	0.996	0.894
977	17	0.953	0.784
978	22	0.982	0.872
979	19	0.890	0.552
980	18	0.984	0.958
981	19	0.981	0.916
982	19	0.995	0.971
983	21	0.980	0.904
984	21	0.980	0.904
985	16	0.961	0.916
986	26	0.951	0.801
987	43	0.992	0.943
988	41	0.937	0.604
989	43	0.994	0.659
990	29	0.986	0.848
991	37	0.984	0.878
992	19	0.942	0.693
993	22	0.982	0.872
995	19	0.993	0.931
996	22	0.992	0.807
997	28	0.990	0.919
998	23	0.896	0.747
999	23	0.985	0.951
1000	21	0.989	0.925
1001	11	0.900	0.758
1002	18	0.933	0.634
1004	16	0.881	0.607

SEQ ID NO:	Position of Signal in Amino Acid SEquence	maxS (Maximum score)	meanS (Mean score)
1005	18	0.964	0.812
1006	19	0.972	0.915
1007	24	0.997	0.929
1008	16	0.945	0.737
1009	31	0.957	0.775
1010	22	0.975	0.822
1011	28	0.946	0.799
1012	24	0.973	0.910
1013	29	0.968	0.769
1014	25	0.977	0.776
1015	41	0.986	0.847
1016	28	0.988	0.938
1017	23	0.976	0.897
1018	45	0.964	0.657
1019	28	0.956	0.604
1020	33	0.948	0.776
1021	18	0.930	0.679
1022	26	0.947	0.594
1023	31	0.991	0.925
1024	41	0.942	0.703
1025	36	0.910	0.749
1026	24	0.988	0.919
1027	27	0.962	0.696
1028	23	0.965	0.693
1029	22	0.962	0.919
1030	24	0.943	0.832
1031	34	0.973	0.817
1032	22	0.947	0.677
1033	25	0.889	0.718
1034	27	0.962	0.856
1035	19	0.967	0.909
1036	39	0.986	0.922
1037	28	0.982	0.924
1038	44	0.974	0.662
1039	29	0.984	0.763
1040	22	0.974	0.796
1041	29	0.928	0.725
1051	23	0.966	0.812
1054	19	0.951	0.895
1055	16	0.927	0.827
1056	25	0.949	0.823
1058	28	0.980	0.848
1061	24	0.965	0.891
1062	25	0.946	0.860
1067	36	0.964	0.648
1074	32	0.941	0.669
1076	17	0.995	0.974
1083	18	0.968	0.799
1089	24	0.882	0.599
1091	38	0.991	0.904
1094	29	0.963	0.888
1096	19	0.892	0.715
1101	34	0.921	0.652
1102	20	0.951	0.839
1106	31	0.921	0.659
1110	36	0.992	0.917
1110	100	0.392	0.917

SEQ ID NO:	Position of Signal in Amino Acid SEquence	maxS (Maximum score)	meanS (Mean score)
1124	30	0.989	0.910
1125	28	0.974	0.851
1127	25	0.937	0.812
1130	30	0.978	0.786
1131	27	0.987	0.879
1133	23	0.923	0.655
1144	28	0.980	0.893
1147	27	0.963	0.833
1150	24	0.976	0.913
1151	24	0.988	0.967
1152	22	0.968	0.831
1154	21	0.952	0.822
1155	42	0.939	0.682
1157	22	0.984	0.928
1158	22	0.984	0.928
1165	21	0.942	0.713
1167	18	0.922	0.838
1170	18	0.988	0.944
1174	18	0.975	0.958
1175	18	0.975	0.958
1176	18	0.975	0.958
1177	48	0.989	0.889
1178	23	0.996	0.936
1180	16	0.967	0.933
1193	15	0.948	0.907
1195	27	0.936	0.689
1196	42	0.978	0.750
1197	15	0.977	0.966
1199 1200	26	0.976	0.875
	28	0.973	0.822
1201 1205	28 22	0.990	0.925
1206	15	0.982	0.933
1207	27	0.994	0.900
1215	21	0.989	0.871
1220	28	0.976	0.653
1226	20	0.987	0.916
1229	30	0.996	0.894
1230	41	0.983	0.791
1234	20	0.978	0.893
1239	17	0.953	0.784
1240	25	0.950	0.897
1241	20	0.974	0.912
1242	15	0.974	0.817
1247	35	0.973	0.795
1250	22	0.982	0.872
1251	18	0.983	0.927
1254	20	0.934	0.828
1255	16	0.952	0.807
1256	19	0.904	0.656
1260	35	0.957	0.640
1261	35	0.957	0.640
1263	33	0.953	0.707
1264	24	0.981	0.884
1265	24	0.987	0.914
1266	21	0.977	0.905

SEQ ID NO:	Position of Signal in Amino Acid SEquence	maxS (Maximum score)	meanS (Mean score)
1267	24	0.978	0.911
1268	18	0.984	0.958
1269	18	0.984	0.958
1270	24	0.989	0.922
1271	18	0.984	0.956
1272	18	0.986	0.965
1273	18	0.986	0.965
1276	32	0.956	0.706
1277	48	0.983	0.616
1278	20	0.965	0.878
1282	16	0.921	0.828
1283	20	0.937	0.700
1293	19	0.995	0.971
1294	19	0.995	0.971
1296	20	0.926	0.751
1302	29	0.981	0.937
1310	27	0.977	0.849
1314	24	0.977	0.845
1315	23	0.990	0.833
1317	25	0.971	0.894
1318	16	0.961	0.916
1319	41	0.980	0.681
1328	17	0.977	0.921
1329	26	0.993	0.894
1331	25	0.986	0.939
1333	33	0.977	0.811
1340	43	0.992	0.943
1341	20	0.943	0.882
1343	20	0.995	0.933
1344	26	0.938	0.663
1346	21	0.955	0.767
1347	19	0.920	0.692
1348	41	0.937	0.604
1349	41	0.937	0.604
1353	19	0.986	0.961
1357	41	0.923	0.559
1359	25	0.973	0.853
1361	20	0.935	0.817
1364	29	0.958	0.637
1365	23	0.991	0.740
1368	29	0.986	0.848
1369	18	0.997	0.979
1373	16	0.979	0.964
1375	25	0.980	0.952
1376	37	0.989	0.822
1378	37	0.984	0.878
1379	42	0.978	0.698
1380	18	0.969	0.913
1383	31	0.981	0.856
1386	36	0.987	0.595
1387	27	0.955	0.786
1389	17	0.915	0.825
1390	34	0.954	0.783
1393	19	0.941	0.839
1396	27	0.944	0.778
1397	20	0.941	0.734

SEQ ID NO:	Position of Signal in Amino Acid SEquence	maxS (Maximum score)	meanS (Mean score)
1404	22	0.982	0.872
1427	19	0.993	0.931
1428	22	0.992	0.807
1430	22	0.918	0.716
1433	38	0.994	0.887
1436	24	0.914	0.588
1438	28	0.990	0.919
1442	26	0.990	0.969
1446	36	0.954	0.817
1450	23	0.896	0.747
1451	23	0.969	0.855
1456	24	0.985	0.932
1462	23	0.985	0.951
1464	27	0.985	0.927
1465	21	0.960	0.649
1467	41	0.990	0.922
1468	20	0.991	0.954
1469	20	0.991	0.954
1473	21	0.975	0.909
1478	11	0.900	0.758
1493	18	0.933	0.634
1495	22	0.899	0.639
1496	40	0.953	0.668
1509	16	0.881	0.607
1516	36	0.924	0.590
1517	25	0.919	0.718
1518	28	0.928	0.590
1519	27	0.967	0.872
1526	25	0.998	0.934
1527	30	0.973	0.829
1547	20	0.937	0.728
1551	30	0.962	0.801
1552	17	0.925	0.779
1557	20	0.981	0.910
1562	17	0.977	0.921
1565	25	0.938	0.677
1568	22	0.975	0.822
1577	34	0.934	0.552
1578	28	0.946	0.799
1583	15	0.954	0.725
1584	30	0.938	0.808
1592	24	0.973	0.910
1597	24	0.920	0.596
1600	29	0.968	0.769
1604	28	0.975	0.926
1613	25	0.977	0.776
1618	41	0.986	0.776
	24		
1627 1630	24	0.915	0.578
1630	28	0.950	0.737 0.785
	19		
1632		0.890	0.552
1633	22	0.968	0.934
1634	22	0.968	0.934
1635	23	0.965	0.883
1636	23	0.965	0.883
1638	26	0.896	0.615

SEQ ID NO:	Position of Signal in Amino Acid SEquence	maxS (Maximum score)	meanS (Mean score)
1641	30	0.956	0.665
1644	39	0.971	0.694
1646	44	0.992	0.576
1649	45	0.964	0.657
1650	45	0.964	0.657
1653	17	0.968	0.947
1655	28	0.960	0.607
1657	31	0.977	0.720
1662	28	0.956	0.604
1666	47	0.985	0.646
1667	19	0.990	0.946
1677	47	0.996	0.556
1684	18	0.930	0.679
1687	25	0.992	0.948
1689	26	0.947	0.594
1693	22	0.963	0.859
1695	26	0.956	0.830
1703	26	0.990	0.959
1706	40	0.987	0.917
1707	26	0.985	0.917
1710	36	0.991	0.868
1713	24	0.887	0.553
1714	23	0.995	0.974
1715	18	0.997	0.977
1716	22	0.968	0.934
1718	26	0.974	0.730
1721	18	0.983	0.939
1731	24	0.988	0.919
1743	30	0.939	0.639
1744	26	0.984	0.746
1755	23	0.965	0.693
1758	22	0.962	0.919
1759	21	0.988	0.911
1760	36	0.980	0.559
1769	10		0.780
1771	14	0.880	
	39		0.678
1773		0.982	0.829
1778	34	0.973	0.817
1779	36	0.976	0.794
1786	18	0.918	0.651
1787	35	0.991	0.834
1789	22	0.947	0.677
1795	24	0.963	0.865
1796	30	0.967	0.758
1797	33	0.926	0.807
1800	25	0.889	0.718
1805	20	0.995	0.968
1807	27	0.887	0.642
1810	41	0.975	0.875
1813	26	0.921	0.620
1826	36	0.951	0.782
1832	19	0.983	0.888
1833	23	0.971	0.941
1834	40	0.964	0.560
1839	39	0.942	0.587
1846	16	0.945	0.737

SEQ ID NO:	Position of Signal in Amino Acid SEquence	maxS (Maximum score)	meanS (Mean score)
1847	24	0.946	0.593
1848	44	0.974	0.662
1850	26	0.974	0.730
1851	27	0.952	0.832
1856	25	0.960	0.642
1866	31	0.956	0.846
1869	16	0.968	0.921
1884	19	0.984	0.936

TABLE 7

SEQ ID	Chromsomal location
1	X
2	Xp21.2-p11.2
3	2
4	2
5	8
6	8
7	17
10	17
13	9
14	Xq24-q25
15	Xq24-q25
16	9p21
17	16
19	7q32
20	2
21	2
22	11
23	12q
27	22q11
28	6p
29	6p23
31	17q
32	12
33	2p23.3-q34
34	9q31-q32
35	19
36	19
37	19q13.3
38	6p21.3
39	10q26.2-10q26.3
40	3
42	12
43	6p21-p12
44	13q12-13
46	2
47	3
48	15q15
49	22q13.33
50	5q14-q22
51	X
52	19cen-q13.2
53	3p26

SEQ ID	Chromsomal location
54	2p24.3
55	3p26
56	3p26
57	15
60	15
62_	1p21.2-22.3
65	11q12-q13.1
66_	xp11
67	20q11.21-q13.12
69 70	2 X
71	1
72	1 1q21.2-q21.3
73	17p11.2
74	X X
75	19
76	9
80	19
83	6q16
85	15
86	12
87	17q22-q24
88	8q22-q23
90	15
91	14q32.3
94	14
95	7
96	10q26.1
97	9p21
98	16q24.3
99	5
101	15
102	19
103	6p21.3
104	11p15.3-p15.4
105	16
107	14q32.1-q32.2
111	11q13
112	9
114	2q35
115	22q13
116	16
117	16
118	16q24.3
120	19
122	1
123	20
124	9
125	3
126	11
127	22q11.2
128	20q11.2-12
129	14
131	10q25.1
133	17p11.2
134	20
136	4p16.3
	978

SEQ ID	Chromsomal location
137	12p13
138	19
139	1p34.1-p32
140	4_or_17
143	Xq13.1-13.3
144	3
145 146	3 5
147	9
148	11q13
149	6
150	15
151	19
152	Xp11.21-11.23
153	18q22-q23
155	16
157	4
160	1p36.23-p33
161	9q22.2
163	4
165	3
166	17
167 168	6p21.3 16
169	9
170	19
171	15
172	2p25
173	22q11.21
174	18q22
179	6p21.3
180	15q14
181	5q
183	5
184	11
187	11
188	3p21.3
189	12p13-gter
190 191	12p13-qter 12p13-qter
191	12p13-qer 12p13-qter
192	2q34-q35
194	2934-935
195	10
199	7q11-q22
200	7q22.1-7q31.33
201	3
202	19q13.4
203	3
205	Xq28
206	6
208	Xq26.2-27.2
209	4
210	4
211	1931
212	19q12-19q13.1
213	6q23
9'	79

214	SEQ ID	Chromsomal location
1952-2342 1913 1921-222 1922-223 1931-223 1931-223 1931-224 1942-225 1	214	
217 8		
1193		
1021-q22 220		
220		
16		1q21-q23
1		
1 1 1 1 1 1 1 1 1 1		
224	223	
225 19p11-q11		
1		
228 1 229 12 230 5 231 1p31-p2.3 232 1p31-p2.3 233 22q12.3 234 22q12.1-q12.3 235 1 236 17 237 15 238 2p13 239 17 241 11p13 242 11 243 4q22-q24 244 12 245 19 246 5 247 14 249 14 250 4 251 19 252 9p2-p21 or 9p13 251 19 252 9p2-p21 or 9p13 256 11q 257 9q3-q34.1 258 13ptc-p13.31 260 1q 261 1q1 262 17 263 12q13 264 <t< td=""><td></td><td>1</td></t<>		1
129	227	
230 5 1931 1931 22.3 1931 1931 22.3 1931 1932 233 2341 235 236 237 238 2241.23 238 2241.24 237 15 238 2913 239 17 241 11913 242 11 14 243 4422.44 12 244 12 245 19 245 19 246 5 5 247 14 249 14 250 4 250 247 248 250 251		
1931 1931 1931 19223 19311-1922.3 19311-1922.3 19311-1922.3 19311-1922.3 19311-1922.3 19311-1922.3 19311-192.3 193		
1931-1-p2.3 1931-1-p2.3 233 2241.23 234 22412.1-q12.3 235 1 1 1 235 1 1 236 1 7 237 15 238 2913 239 17 7 241 11 11 12 244 11 11		
233 22011.23 22012.3 22012.3 2212.3 2225 1		
220 1 1 1 2 2 2 2 2 2 2		
235		
236		
15		
238 2013 239 17 241 11p13 242 11 243 4022-024 244 12 245 19 246 5 247 14 248 16 249 14 250 4 251 19 252 9922-p21 or 9p13 256 11q 257 9933-934.1 258 12pter-p13.31 260 8 261 11q14 262 17 263 12q13 264 16q13-q21 265 16q13-q21 266 16q13-q21 267 6q65-27 268 9q12-q21.2 269 9q12-q21.2 270 9q12-q21.2 271 19 272 1p41-35.3 273 11 274 11 <t< td=""><td></td><td></td></t<>		
241		
242	239	17
243		
244 12 245 19 246 5 5 247 14 4 248 16 250 4 250 4 251 252		
245 19 246 5 247 14 248 16 249 14 250 4 251 19 252 9p22-p21 or 9p13 256 11c 257 9q33-q34.1 258 12pter-p13.31 260 8 8 8 261 11q14 262 17 263 12q13 264 16q13-q21 265 16q13-q21 267 6q26-27 268 9q12-q21.2 269 9q12-q21.2 270 9q12-q21.2 271 19 272 1p341-35.3 273 111 274 11 275 X 277 2		
246 5 14 248 16 249 14 250 4 251 19 252 262 262 271 268 268 268 269		
247		
248 16 249 14 250 4 251 19 252 9p22-p21 or 9p13 256 11q 257 9q33-q34.1 258 12pterp13.31 260 8 261 11q14 262 17 263 12q13 264 16q13-q21 265 16q13-q21 266 6p2-27 268 9q12-q21.2 269 9q12-q21.2 270 9q12-q21.2 271 19 272 1p34.1-35.3 273 11 273 11 274 11 275 X 277 2		
249 14 250 4 251 19 252 9p22-p21 or 9p13 256 11q 257 9q33-q34.1 258 12pter-p13.31 260 8 261 11q14 262 17 263 12q13 264 16q13-q21 265 16q13-q21 267 6q26-27 268 9q12-q21.2 269 9q12-q21.2 270 9q12-q21.2 271 19 272 1p34.1-35.3 273 11 274 11 275 X 277 2		
250 4 19 19 251 19 252 264 265		
252 9922-921 or 9p13		
256 11q 257 9q33-q34.1 258 12pter-p13.31 260 8 261 11q14 262 17 263 12q13 264 16q13-q21 265 16q13-q21 267 6q5c-27 268 9q12-q1.2 269 9q12-q21.2 270 3q12-q21.2 271 19 272 1p341-35.3 273 11 274 11 275 X 277 2	251	19
257 9433-q34.1 258 12pter-p13.31 260 8 261 11q14 262 1/7 263 12q13 264 16q13-q21 265 16q13-q21 267 6q26-27 268 9412-q21.2 269 9412-q21.2 270 9412-q21.2 270 9412-q21.3 271 19 272 1p34.1-35.3 274 11 275 X 277 2		
258 12pter-p13.31 260 8 261 11q14 262 17 263 12q13 264 16q13-q21 265 16q13-q21 267 6g6-27 268 9q12-q21.2 269 3q12-q21.2 270 3q12-q21.2 271 19 272 1p34.1-35.3 273 11 274 11 275 X 277 2		
260 8 261 11q14 262 17 263 12q13 264 16q13-q21 265 16q13-q21 267 6q26-27 268 9q12-q21.2 269 9q12-q21.2 270 9q12-q21.2 271 19 272 1p34,1-35.3 273 11 274 11 275 X 2777 2		
261 11q14 262 17 263 12q13 264 16q13-q21 265 16q13-q21 267 6q5c-27 268 9q12-q1.2 269 9q12-q21.2 270 3q12-q21.2 271 19 272 1p341-35.3 273 11 274 11 275 X 277 2		
262 17 263 12q13 264 16q13-q21 265 16q13-q21 267 6q26-27 268 9q12-q21.2 269 9q12-q21.2 270 9q12-q21.2 271 19 272 1p34.1-35.3 273 11 274 11 275 X 277 2		
263 12q13 264 16q13-q21 265 16q13-q21 267 6q5c-27 268 9q12-q1.2 269 9q12-q1.2 270 3q12-q1.2 271 19 272 1p34.1-35.3 273 11 274 11 275 X 277 2		
264 16q13-q21 265 16q13-q21 267 6q25-27 268 9q12-q21.2 269 9q12-q21.2 270 9q12-q21.2 271 19 272 1p34,1-35,3 273 11 274 11 275 X 277 2		
265 16q13-q21 267 6q2c-27 268 9q12-q21.2 269 9q12-q21.2 270 9q12-q21.2 271 19 272. 1p34.1-35.3 273 11 274 11 275 X 277 2		
267 6q25-27 268 9q12-q21.2 269 9q12-q21.2 270 9q12-q21.2 271 19 272 1p34.1-35.3 273 11 274 11 275 X 277 2		
268 9012-Q21.2 269 9012-Q21.2 270 9q12-Q21.2 271 19 272 1p34.1-35.3 273 11 274 11 275 X 277 2		
269 9q12-q21.2 270 9q12-q21.2 271 19 272 1p34.1-35.3 273 11 274 11 275 X 277 2		9q12-q21.2
270 9q12-q21.2 271 19 272 1p34.1-35.3 273 11 274 11 275 X 277 2		9q12-q21.2
271 19 272 1p34.1-35.3 273 11 274 11 275 X 277 2		9q12-q21.2
273 11 274 11 275 X 277 2		19
274 11 275 X 277 2	272	
275 X 277 2		
277 2		
	211	

SEQ ID	Chromsomal location
278	16
280	19q13.1-q13.2
282	12
284	2p23.3-q24.3
285	11p15
286	19
287	7
288	10
290	12
293	3q23-q24
294	1p34.1-35.3
295	p22.2-31.1
296	3q22-q24
297	6
299	2p11
300	16
301	10q24
302	10
304	12q22-q23
305	17pter-p11
307 308	1p35-p34
309	16 21
310	12p13
312	1
313	1
314	17
315	1942-943
316	6p21.32-22.1
317	6p21.32-22.1
318	6p21.32-22.1
319	6p21.32-22.1
320	6p21.32-22.1
321	6p21.32-22.1
322	6p21.32-22.1
323	6p21.32-22.1
324	6p21.32-22.1
325	6p21.32-22.1
326	17
327	3
328	14
332	17
335	17
336	14q32
337	8q23
338	8q23
339	16q11.1-q11.2
340	8q22-q23
341	16p13.3
342	18
343	15
344	17
345	20q11.2-q13.1
346	20q11.2-q13.1
347	19q13.3
348	19
	R1

SEQ ID	Chromsomal location
349	17q25.1
350	18
351	11
352	1
353	q25.1-31.1
354	11914
355	1q31
356	1q31
357	18
358	3p
359	10
360	7922
361	7q22
362	1q21.3
363	3
364	18q12
365	11p15
367	14
369	1p36.21
371	6p12.3-21.1
373	14q13.1-14q21.3
374	15
375	4
376	7q32-q34
377	7q32-q34
378	20q13.1-q13.2
381	13
382	1921.2-22
383	16
384 385	12
386	20q13.1
387	8q21.3-q22.1
388	11
389	15q22.1
390	17
391	17
394	8q23
395	15q24-q26
396	15q22
397	7q34-q36
399	2
400	6q21-22
401	6q21-22
402	14q24.3
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404	11q13
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407	14
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409	10q23-q24
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411	11
412	11p15
413	12q13.2-q13.3
414	3p13-q26.1
416	17

SEQ ID	Chromsomal location
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426	6p21.1-21.2
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429	11
430	2
432	14q31
433	17
434	22
436	7q35
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441	11q12
443	5
444	1
445	13q13
446	17
447	17
448	1p35.2-36.13
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450	15q24-q25
451	19
452	4
453	2
454	11
455	17
456	10
457	p31.3-32.2
458	1
459	7p13-p11.2
460	12
461	18p11.2
462	17
463	22q11.2
464	16
466	17
467	11q23
468	3
469	7q32
470	1
472	19
473	19
474	p33-34.3
475	7436
476	2
477	9p24.1-24.3
478	6p22.1-22.3
479	20
480	22912.3-13.1
481	16q22.1-q22.3
483	19
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771	1q21-q22 983

492	SEQ ID	Chromsomal location
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497		
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11q 499	497	17q23.2-q25.3
10		11q
Section Sect		4p15.31
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11p15.5		
11		
510 15q25 511 14q21q22.3 512 13q11 513 10 514 Xq28 515 15q15 516 19p13.3 518 14q21 00000385Rd232 1 519 13 520 12 521 12 522 20q12-q13.12 523 6q22.1-22.33 524 12 526 16 527 17 528 3 530 1q42.13-43 51 16p 532 17 533 16q24.1 534 19p13.p13.2 535 19p13.3-p13.2 536 13 537 17 539 1q21.2-q22 540 17 541 18q12 542 16 537 17 539 1q21.2-q22		
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542 16 545 3p23.3-q34 546 14q21.1-q22.3 547 2p12 548 17q11-qter 549 4 550 17 551 9 552 17q24-q25		
545 2p23.3-q34 546 14q21.1-q22.3 547 2p12 548 17q11-qter 549 4 550 17 551 9 552 17q24-q25		
546 14q21.1-q22.3 547 2p12 548 17q11-qter 549 4 550 17 551 9 552 17q24-q25		
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574	6p11.2-12.3
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577	12
578	17
579	10
580	6p21
581	2
582	3q25.1-q25.2
583	3q25.1-q25.2
584	19
585	19p13.3
586	15
587	15
588	4q25
589	9p24
590	17
591	20q13.11-13.2
592	x
593	2p23.3-q24.3
594	6p22.1
595	1
596	
597	2q31-q37
598	1p36.1
599	2p11.2-q11.2
600	19p13.1
601	2
602	17p13.3
603	15q
604	11
606	1p36
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613	12
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616	20q11.2
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SEQ ID	Chromsomal location
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631	20
632	20
634	16
636	16
637	2
638	20q13
639	8q22-q23
640	8
642	5q21-q22
643	xq26
644	22
645	11q25
646	2
647	2p23.3-q34
648	5
651	X
652	3
653	3p13-q26.1
654	12q
655	12q
656	17
657	17
658	12
659	12
660	9q31
661	11
663	6
664	2p23.3-q24.3
666	10
667	219
668	11
669	11
670	21q22.3
671	4p16.1
672 673	11 12
675	19
676	19
677	6p24-25
678	5 5
679	x
680	3p21.1-q12.3
681	5
683	12p13.1-p12,3
684	17q
g	986

SEQ ID	Chromsomal location
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697	7p14.3-p14.1
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699	18q12-q21
700	14q24.3
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702	17
703	i'
704	20p13
705	6pter-p21.1
706	17
708	8
711	1
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713	16
714	18q21
715	17
716	1932
717	1q12-21.1
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723	11
724	5
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727	17q21.3
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730	12
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732	12
733	15q15
734	8q24.3
735	Xq26.3-27.3
736	19q13.2
737	21q22.1
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742	1p36.2-p35
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748	2p23
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750	4
751	17p11.2
752	1p13

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756	5pter-p13.3
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758	19q13
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762	19
763	X
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766	9q34.3
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783	19q13.4
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786	8
787	17
788 789	8 1q42.13-43
790	7q11.21-q11.23
790	7q11.21-q11.23
792	3p13-q13.2
793	9
794	11q12
795	1p32.2-34.2
797	18
798	18
799	11q13
800	17
801	7p15-p21
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803	17p13.1
805	17q25.3
806	17q25
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SEQ ID	Chromsomal location
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825	1p32.3
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828	p34.1-34.3
829	16
830	8p11.2
831	17g21.3-17g22
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834	7p
835	21
836	10cen-q26.11
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838	5
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845	17
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847	17
848	10
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858	16
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863	18p11.2
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866	15q15
867	7
868	12
869	1
870	11g23
871	16
872	16p13.3
873	17q12-q21
874	11q13.5
875	11cen-q12.1
876	16q13
877	X
878	1q21-q23
879	xq22.1-q22.3
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SEQ ID	Chromsomal location
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890	13
891	17
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893	6p21.32-22.2
894	11
895	7q33-q34
897	13
898	15
901	1
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904	16p11.2
905	21q22.3
907	10
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910	10q26
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913	18
914	6
915	10
916	13
917	17
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929	2q21 19
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932	16
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TABLE 8

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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52	1000	52
53	1001	53
54	1002	54

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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60	1008	60
61	1009	61
62	1010	62
63	1011	63
64	1012	64
65	1013	65
66	1014	66
67	1015	67
68	1016	68
69	1017	69
70	1018	70
71	1019	71
72	1020	72
73	1021	73
74	1022	74
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76	1024	76
77	1025	77
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82	1030	82
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84	1032	84
85	1033	85
86	1034	86
87	1035	87
88	1036	88
89	1037	89
90	1038	90
91	1039	91
92	1040	92
93	1041	93
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SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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120	1068	120
121	1069	121
123	1070	122
124	1071	123
125	1072 1073	124 125
126		
127	1074 1075	126 127
128	1076	127
129	1077	128
130	1078	130
131	1079	131
132	1080	132
133	1081	133
134	1082	134
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138	1086	138
139	1087	139
140	1088	140
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142	1090	142
143	1091	143
144	1092	144
145	1093	145
146	1094	146
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149	1097	149
150	1098	150
151	1099	151
152	1100	152
153	1101	153
154	1102	154
155	1103	155
156	1104	156
157	1105	157
158	1106	158
159	1107	159
160	1108	160
161	1109	161
162	1110	162
163	1111	163
164	1112	164
165 166	1113	165
100	1114	166

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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169	1117	169
170	1118	170
171	1119	171
172	1120	172
173	1121	173
174	1122	174
175	1123	175
176 177	1124 1125	176
178	1125	178
179	1127	179
180	1128	180
181	1129	181
182	1130	182
183	1131	183
184	1132	184
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186	1134	186
187	1135	187
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197 198	1145 1146	197
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214	1162	214
215	1163	215
216	1164	216
217	1165	217
218	1166	218
219	1167	219
220	1168	220
221	1169	221
222	1170	222

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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226	1174	226
227	1175	227
228	1176	228
229	1177	229
230	1178	230
231	1179	231
232	1180	232
233	1181	233
234	1182	234
235	1183	235
236	1184	236
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238	1186	238
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244	1192	244
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247	1195	247
248	1196	248
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263	1211	263
264	1212	264
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SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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318	1266	318
319	1267	319
320	1268	320
321	1269	321
322	1270	322
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324	1272	324
325	1273	325
326	1274	326
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329	1277	329
330	1277	330
331	1279	331
332	1280	332
333	1281	333
334	1282	334
754	1202	1 334

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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340	1288	340
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354	1302	354
355	1303	355
356	1304	356
357	1305	357
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363	1311	363
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369	1317	369
370	1318	370
371	1319	371
372	1320	372
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377	1325	377
378	1326	378
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380	1328	380
381	1329	381
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383	1331	383
384	1332	384
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387	1335	387
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390	1338	390
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SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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426	1374	426
427	1375	426
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430	1378 1379	430
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444	1392	444
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446	1394	446

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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454	1402	454
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474	1422	474
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484	1432	484
485	1433	485
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SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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522	1470	522
523	1471	523
524	1472	524
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532	1480	532
533	1481	533
534	1482	534
535	1483	535
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SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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574	1522	574
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614	1561 1562	613
014	1302	614

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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622	1570	622
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624	1572	624
625	1573	625
626	1574	626
627	1575	627
628	1576	628
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630	1578	630
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633	1581	633
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635	1583	635
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637	1585	637
638	1586	638
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670	1618	670

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799.451
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699	1647	699
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701	1649	701
702	1650	702
703	1651	703
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711	1659	711
712	1660	712
713	1661	713
714	1662	714
715	1663	715
716	1664	716
717	1665	717
718	1666	718
719	1667	719
720	1668	720
721	1669	721
722	1670	722
723	1671	723
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725	1673	724

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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733	1681	733
734	1682	734
735	1683	735
736	1684	736
737	1685	737
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743	1691	743
744	1692	744
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748	1696	748
749	1697	749
750	1698	750
751	1699	751
752 753	1700 1701	752 753
754	1702	754
755	1703	
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757	1705	757
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763	1711	763
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765	1713	765
766	1714	766
767	1715	767
768	1716	768
769	1717	769
770	1718	770
771	1719	771
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774	1722	774
775	1723	775
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781	1729	781
782	1730	782

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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792	1740	792
793	1741	793
794	1742	794
795	1743	795
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797	1745	797
798	1746	798
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802	1750	802
803	1751	803
804	1752	804
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809	1757	809
810	1758	810
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812	1760	812
813	1761	813
814	1762	814
815	1763	815
816	1764	816
817	1765	817
818	1766	818
819	1767	819
820	1768	820
821	1769	821
822	1770	822
823	1771	823
824	1772	824
825	1773	825
826	1774	826
827	1775	827
828	1776	828
829	1777	829
830	1778	830
831	1779	831
832	1780	832
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836	1784	836
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838	1786	838

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799,451
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849	1797	849
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855	1803	854
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877	1825	877
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879	1827	879
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881	1829	881
882 883	1830	882
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885	1833	885
886	1834	886
887	1835	887
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894	1842	894
	1006	

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 09/799.451
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899	1847	899
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901	1849	901
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905	1853	905
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	1855	907
908	1856 1857	908
910	1858	910
911	1859	911
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914	1862	914
915	1863	915
916	1864	916
917	1865	917
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919	1867	919
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930	1878	930
931	1879	931
932	1880	932
933	1881	933
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941	1889	941
942	1890	942
943	1891	943
944	1892	944
	1893	945
946	1894	946
947	1895 1896	947
740	1090	948

CLAIMS

WHAT IS CLAIMED IS:

- An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1 – 948, a mature protein coding portion of SEQ ID NO: 1 – 948, an active domain coding protein of SEQ ID NO: 1 – 948, and complementary sequences thereof.
- An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
 - 3. The polynucleotide of claim 1 wherein said polynucleotide is DNA.

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- An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
- A vector comprising the polynucleotide of claim 1.

- An expression vector comprising the polynucleotide of claim 1.
- A host cell genetically engineered to comprise the polynucleotide of claim 1.
- 8. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
- An isolated polypeptide, wherein the polypeptide is selected from the group consisting
 of a polypeptide encoded by any one of the polynucleotides of claim 1 (i.e. SEQ ID NO: 949-1896).
 - 10. A composition comprising the polypeptide of claim 9 and a carrier.

11. An antibody directed against the polypeptide of claim 9.

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- 12. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample with a compound that binds to and forms a
 complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and
- b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.
- 13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;
- b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and
- c) detecting said product and thereby the polynucleotide of claim 1 in the sample.
- 14. The method of claim 13, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.
- 15. A method for detecting the polypeptide of claim 9 in a sample, comprising:
- a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and
 - b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 9 is detected.
- 16. A method for identifying a compound that binds to the polypeptide of claim 9, 30 comprising:
 - a) contacting the compound with the polypeptide of claim 9 under eonditions sufficient to form a polypeptide/compound complex; and
 - b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 9 is identified.

17. A method for identifying a compound that binds to the polypeptide of claim 9, comprising:

- a) contacting the compound with the polypeptide of claim 9, in a cell,
 under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and
 - b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 9 is identified.

18. A method of producing the polypeptide of claim 9, comprising,

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- a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO: 1-948, a mature protein coding portion of SEQ ID NO: 1-948, an active domain coding portion of SEQ ID NO: 1-948, complementary sequences thereof, under conditions sufficient to express the polypeptide in said cell; and
 - b) isolating the polypeptide from the cell culture or cells of step (a).
- 19. An isolated polypeptide comprising an amino acid sequence selected from the group 20 consisting of any one of the polypeptides from the Sequence Listing, the mature protein portion thereof, or the active domain thereof.
 - The polypeptide of claim 21 wherein the polypeptide is provided on a polypeptide array.
 - A collection of polynucleotides, wherein the collection comprising the sequence information of at least one of SEQ ID NO: 1 – 948.
 - 22. The collection of claim 21, wherein the collection is provided on a nucleic acid array.
 - The collection of claim 22, wherein the array detects full-matches to any one of the
 polynucleotides in the collection.

24. The collection of claim 22, wherein the array detects mismatches to any one of the polynucleotides in the collection.

 The collection of claim 21, wherein the collection is provided in a computer-readable format

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- 26. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 9 or 19 and a pharmaceutically acceptable carrier.
- 27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 9 or 19 and a pharmaceutically acceptable carrier.